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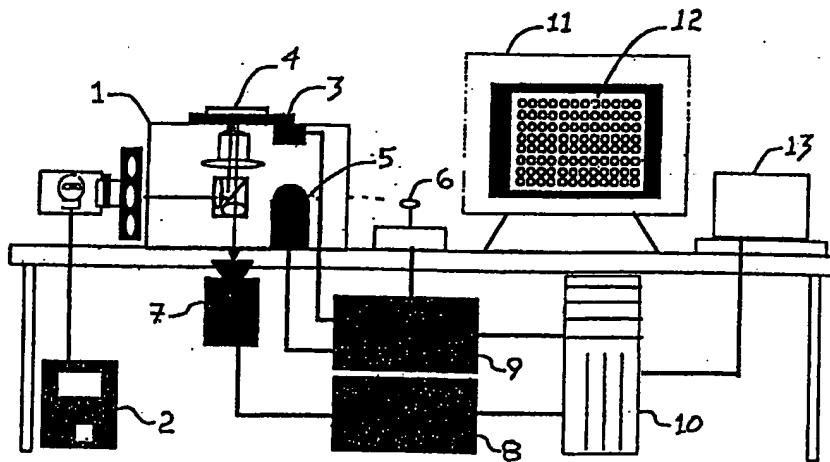


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(54) Title: A SYSTEM FOR CELL-BASED SCREENING



(57) Abstract

The present invention provides systems, methods, screens, reagents and kits for optical system analysis of cells to rapidly determine the distribution, environment, or activity of fluorescently labeled reporter molecules in cells for the purpose of screening large numbers of compounds for those that specifically affect particular biological functions.

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A SYSTEM FOR CELL-BASED SCREENING

5 Cross Reference

This application claims priority to U.S. Provisional Applications for Patent Serial Nos. 60/122,152 (February 26, 1999), 60/123,399 (March 8, 1999), 09/352,141, (July 12, 1999), 60/151,797 (August 31, 1999), 60/168,408 (December 1, 1999); and is a continuation in part of 09/430,656 (October 29, 1999); 09/398,965 filed September 10 17, 1999 which is a continuation in part of Serial No. 09/031,271 filed February 27, 1998 which is a continuation in part of U.S. Application S/N 08/810983, filed on February 27, 1997.

Field of The Invention

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This invention is in the field of fluorescence-based cell and molecular biochemical assays for drug discovery.

Background of the Invention

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Drug discovery, as currently practiced in the art, is a long, multiple step process involving identification of specific disease targets, development of an assay based on a specific target, validation of the assay, optimization and automation of the assay to produce a screen, high throughput screening of compound libraries using the assay to identify "hits", hit validation and hit compound optimization. The output of this process is a lead compound that goes into pre-clinical and, if validated, eventually into clinical trials. In this process, the screening phase is distinct from the assay development phases, and involves testing compound efficacy in living biological systems.

25

Historically, drug discovery is a slow and costly process, spanning numerous years and consuming hundreds of millions of dollars per drug created. Developments in the areas of genomics and high throughput screening have resulted in increased capacity and efficiency in the areas of target identification and volume of compounds

Historically, drug discovery is a slow and costly process, spanning numerous years and consuming hundreds of millions of dollars per drug created. Developments in the areas of genomics and high throughput screening have resulted in increased capacity and efficiency in the areas of target identification and volume of compounds screened. Significant advances in automated DNA sequencing, PCR application, positional cloning, hybridization arrays, and bioinformatics have greatly increased the number of genes (and gene fragments) encoding potential drug screening targets. However, the basic scheme for drug screening remains the same.

Validation of genomic targets as points for therapeutic intervention using the existing methods and protocols has become a bottleneck in the drug discovery process due to the slow, manual methods employed, such as *in vivo* functional models, functional analysis of recombinant proteins, and stable cell line expression of candidate genes. Primary DNA sequence data acquired through automated sequencing does not permit identification of gene function, but can provide information about common "motifs" and specific gene homology when compared to known sequence databases. Genomic methods such as subtraction hybridization and RADE (rapid amplification of differential expression) can be used to identify genes that are up or down regulated in a disease state model. However, identification and validation still proceed down the same pathway. Some proteomic methods use protein identification (global expression arrays, 2D electrophoresis, combinatorial libraries) in combination with reverse genetics to identify candidate genes of interest. Such putative "disease associated sequences" or DAS isolated as intact cDNA are a great advantage to these methods, but they are identified by the hundreds without providing any information regarding type, activity, and distribution of the encoded protein. Choosing a subset of DAS as drug screening targets is "random", and thus extremely inefficient, without functional data to provide a mechanistic link with disease. It is necessary, therefore, to provide new technologies to rapidly screen DAS to establish biological function, thereby improving target validation and candidate optimization in drug discovery.

There are three major avenues for improving early drug discovery productivity. First, there is a need for tools that provide increased information handling capability. Bioinformatics has blossomed with the rapid development of DNA sequencing systems and the evolution of the genomics database. Genomics is beginning to play a critical

role in the identification of potential new targets. Proteomics has become indispensable in relating structure and function of protein targets in order to predict drug interactions. However, the next level of biological complexity is the cell. Therefore, there is a need to acquire, manage and search multi-dimensional information from cells. Secondly, 5 there is a need for higher throughput tools. Automation is a key to improving productivity as has already been demonstrated in DNA sequencing and high throughput primary screening. The instant invention provides for automated systems that extract multiple parameter information from cells that meet the need for higher throughput tools. The instant invention also provides for miniaturizing the methods, thereby 10 allowing increased throughput, while decreasing the volumes of reagents and test compounds required in each assay.

Radioactivity has been the dominant read-out in early drug discovery assays. However, the need for more information, higher throughput and miniaturization has caused a shift towards using fluorescence detection. Fluorescence-based reagents can 15 yield more powerful, multiple parameter assays that are higher in throughput and information content and require lower volumes of reagents and test compounds. Fluorescence is also safer and less expensive than radioactivity-based methods.

Screening of cells treated with dyes and fluorescent reagents is well known in the art. There is a considerable body of literature related to genetic engineering of cells 20 to produce fluorescent proteins, such as modified green fluorescent protein (GFP), as a reporter molecule. Some properties of wild-type GFP are disclosed by Morise et al. (*Biochemistry* 13 (1974), p. 2656-2662), and Ward et al. (*Photochem. Photobiol.* 31 (1980), p. 611-615). The GFP of the jellyfish *Aequorea victoria* has an excitation maximum at 395 nm and an emission maximum at 510 nm, and does not require an 25 exogenous factor for fluorescence activity. Uses for GFP disclosed in the literature are widespread and include the study of gene expression and protein localization (Chalfie et al., *Science* 263 (1994), p. 12501-12504)), as a tool for visualizing subcellular organelles (Rizzuto et al., *Curr. Biology* 5 (1995), p. 635-642)), visualization of protein transport along the secretory pathway (Kaether and Gerdes, *FEBS Letters* 369 (1995), 30 p. 267-271)), expression in plant cells (Hu and Cheng, *FEBS Letters* 369 (1995), p. 331-334)) and Drosophila embryos (Davis et al., *Dev. Biology* 170 (1995), p. 726-729)), and as a reporter molecule fused to another protein of interest (U. S. Patent

5,491,084). Similarly, WO96/23898 relates to methods of detecting biologically active substances affecting intracellular processes by utilizing a GFP construct having a protein kinase activation site. This patent, and all other patents referenced in this application are incorporated by reference in their entirety.

5 Numerous references are related to GFP proteins in biological systems. For example, WO 96/09598 describes a system for isolating cells of interest utilizing the expression of a GFP like protein. WO 96/27675 describes the expression of GFP in plants. WO 95/21191 describes modified GFP protein expressed in transformed organisms to detect mutagenesis. U. S. Patents 5,401,629 and 5,436,128 describe
10 assays and compositions for detecting and evaluating the intracellular transduction of an extracellular signal using recombinant cells that express cell surface receptors and contain reporter gene constructs that include transcriptional regulatory elements that are responsive to the activity of cell surface receptors.

15 Performing a screen on many thousands of compounds requires parallel handling and processing of many compounds and assay component reagents. Standard high throughput screens ("HTS") use mixtures of compounds and biological reagents along with some indicator compound loaded into arrays of wells in standard microtiter plates with 96 or 384 wells. The signal measured from each well, either fluorescence emission, optical density, or radioactivity, integrates the signal from all the material in
20 the well giving an overall population average of all the molecules in the well.

Science Applications International Corporation (SAIC) 130 Fifth Avenue, Seattle, WA. 98109) describes an imaging plate reader. This system uses a CCD camera to image the whole area of a 96 well plate. The image is analyzed to calculate the total fluorescence per well for all the material in the well.

25 Molecular Devices, Inc. (Sunnyvale, CA) describes a system (FLIPR) which uses low angle laser scanning illumination and a mask to selectively excite fluorescence within approximately 200 microns of the bottoms of the wells in standard 96 well plates in order to reduce background when imaging cell monolayers. This system uses a CCD camera to image the whole area of the plate bottom. Although this system
30 measures signals originating from a cell monolayer at the bottom of the well, the signal measured is averaged over the area of the well and is therefore still considered a measurement of the average response of a population of cells. The image is analyzed to

calculate the total fluorescence per well for cell-based assays. Fluid delivery devices have also been incorporated into cell based screening systems, such as the FLIPR system, in order to initiate a response, which is then observed as a whole well population average response using a macro-imaging system.

- 5 In contrast to high throughput screens, various high-content screens ("HCS") have been developed to address the need for more detailed information about the temporal-spatial dynamics of cell constituents and processes. High-content screens automate the extraction of multicolor fluorescence information derived from specific fluorescence-based reagents incorporated into cells (Giuliano and Taylor (1995), *Curr.*
10 *Op. Cell Biol.* 7:4; Giuliano et al. (1995) *Ann. Rev. Biophys. Biomol. Struct.* 24:405). Cells are analyzed using an optical system that can measure spatial, as well as temporal dynamics. (Farkas et al. (1993) *Ann. Rev. Physiol.* 55:785; Giuliano et al. (1990) In *Optical Microscopy for Biology*. B. Herman and K. Jacobson (eds.), pp. 543-557. Wiley-Liss, New York; Hahn et al (1992) *Nature* 359:736; Waggoner et al. (1996)
15 *Hum. Pathol.* 27:494). The concept is to treat each cell as a "well" that has spatial and temporal information on the activities of the labeled constituents.

- The types of biochemical and molecular information now accessible through fluorescence-based reagents applied to cells include ion concentrations, membrane potential, specific translocations, enzyme activities, gene expression, as well as the
20 presence, amounts and patterns of metabolites, proteins, lipids, carbohydrates, and nucleic acid sequences (DeBiasio et al., (1996) *Mol. Biol. Cell.* 7:1259; Giuliano et al., (1995) *Ann. Rev. Biophys. Biomol. Struct.* 24:405; Heim and Tsien, (1996) *Curr. Biol.* 6:178).

- High-content screens can be performed on either fixed cells, using fluorescently
25 labeled antibodies, biological ligands, and/or nucleic acid hybridization probes, or live cells using multicolor fluorescent indicators and "biosensors." The choice of fixed or live cell screens depends on the specific cell-based assay required.

- Fixed cell assays are the simplest, since an array of initially living cells in a microtiter plate format can be treated with various compounds and doses being tested,
30 then the cells can be fixed, labeled with specific reagents, and measured. No environmental control of the cells is required after fixation. Spatial information is acquired, but only at one time point. The availability of thousands of antibodies,

ligands and nucleic acid hybridization probes that can be applied to cells makes this an attractive approach for many types of cell-based screens. The fixation and labeling steps can be automated, allowing efficient processing of assays.

Live cell assays are more sophisticated and powerful, since an array of living
5 cells containing the desired reagents can be screened over time, as well as space. Environmental control of the cells (temperature, humidity, and carbon dioxide) is required during measurement, since the physiological health of the cells must be maintained for multiple fluorescence measurements over time. There is a growing list of fluorescent physiological indicators and "biosensors" that can report changes in
10 biochemical and molecular activities within cells (Giuliano et al., (1995) *Ann. Rev. Biophys. Biomol. Struct.* 24:405; Hahn et al., (1993) In *Fluorescent and Luminescent Probes for Biological Activity*. W.T. Mason, (ed.), pp. 349-359, Academic Press, San Diego).

The availability and use of fluorescence-based reagents has helped to advance
15 the development of both fixed and live cell high-content screens. Advances in instrumentation to automatically extract multicolor, high-content information has recently made it possible to develop HCS into an automated tool. An article by Taylor, et al. (*American Scientist* 80 (1992), p. 322-335) describes many of these methods and their applications. For example, Proffitt et. al. (*Cytometry* 24: 204-213 (1996)) describe
20 a semi-automated fluorescence digital imaging system for quantifying relative cell numbers *in situ* in a variety of tissue culture plate formats, especially 96-well microtiter plates. The system consists of an epifluorescence inverted microscope with a motorized stage, video camera, image intensifier, and a microcomputer with a PC-Vision digitizer. Turbo Pascal software controls the stage and scans the plate taking
25 multiple images per well. The software calculates total fluorescence per well, provides for daily calibration, and configures easily for a variety of tissue culture plate formats. Thresholding of digital images and reagents which fluoresce only when taken up by living cells are used to reduce background fluorescence without removing excess fluorescent reagent.

30 Scanning confocal microscope imaging (Go et al., (1997) *Analytical Biochemistry* 247:210-215; Goldman et al., (1995) *Experimental Cell Research* 221:311-319) and multiphoton microscope imaging (Denk et al., (1990) *Science*

248:73; Gratton et al., (1994) *Proc. of the Microscopical Society of America*, pp. 154-155) are also well established methods for acquiring high resolution images of microscopic samples. The principle advantage of these optical systems is the very shallow depth of focus, which allows features of limited axial extent to be resolved
5 against the background. For example, it is possible to resolve internal cytoplasmic features of adherent cells from the features on the cell surface. Because scanning multiphoton imaging requires very short duration pulsed laser systems to achieve the high photon flux required, fluorescence lifetimes can also be measured in these systems (Lakowicz et al., (1992) *Anal. Biochem.* 202:316-330; Gerritsen et al. (1997), *J. of*
10 *Fluorescence* 7:11-15)), providing additional capability for different detection modes. Small, reliable and relatively inexpensive laser systems, such as laser diode pumped lasers, are now available to allow multiphoton confocal microscopy to be applied in a fairly routine fashion.

A combination of the biological heterogeneity of cells in populations (Bright, et
15 al., (1989). *J. Cell. Physiol.* 141:410; Giuliano, (1996) *Cell Motil. Cytoskel.* 35:237)) as well as the high spatial and temporal frequency of chemical and molecular information present within cells, makes it impossible to extract high-content information from populations of cells using existing whole microtiter plate readers. No existing high-content screening platform has been designed for multicolor, fluorescence-based
20 screens using cells that are analyzed individually. Similarly, no method is currently available that combines automated fluid delivery to arrays of cells for the purpose of systematically screening compounds for the ability to induce a cellular response that is identified by HCS analysis, especially from cells grown in microtiter plates. Furthermore, no method exists in the art combining high throughput well-by-well
25 measurements to identify "hits" in one assay followed by a second high content cell-by-cell measurement on the same plate of only those wells identified as hits.

The instant invention provides systems, methods, and screens that combine high throughput screening (HTS) and high content screening (HCS) that significantly improve target validation and candidate optimization by combining many cell screening
30 formats with fluorescence-based molecular reagents and computer-based feature extraction, data analysis, and automation, resulting in increased quantity and speed of

data collection, shortened cycle times, and, ultimately, faster evaluation of promising drug candidates. The instant invention also provides for miniaturizing the methods, thereby allowing increased throughput, while decreasing the volumes of reagents and test compounds required in each assay.

5

SUMMARY OF THE INVENTION

In one aspect, the present invention relates to a method for analyzing cells comprising providing cells containing fluorescent reporter molecules in an array of locations, treating the cells in the array of locations with one or more reagents, 10 imaging numerous cells in each location with fluorescence optics, converting the optical information into digital data, utilizing the digital data to determine the distribution, environment or activity of the fluorescently labeled reporter molecules in the cells and the distribution of the cells, and interpreting that information in terms of a positive, negative or null effect of the compound being tested on the biological 15 function

In this embodiment, the method rapidly determines the distribution, environment, or activity of fluorescently labeled reporter molecules in cells for the purpose of screening large numbers of compounds for those that specifically affect particular biological functions. The array of locations may be a microtiter plate or a 20 microchip which is a microplate having cells in an array of locations. In a preferred embodiment, the method includes computerized means for acquiring, processing, displaying and storing the data received. In a preferred embodiment, the method further comprises automated fluid delivery to the arrays of cells. In another preferred embodiment, the information obtained from high throughput measurements on the 25 same plate are used to selectively perform high content screening on only a subset of the cell locations on the plate.

In another aspect of the present invention, a cell screening system is provided that comprises:

- a high magnification fluorescence optical system having a microscope objective,

30

- an XY stage adapted for holding a plate containing an array of cells and having a means for moving the plate for proper alignment and focusing on the cell arrays;
- a digital camera;
- 5 • a light source having optical means for directing excitation light to cell arrays and a means for directing fluorescent light emitted from the cells to the digital camera; and
- a computer means for receiving and processing digital data from the digital camera wherein the computer means includes a digital frame grabber for receiving the images from the camera, a display for user interaction and display of assay results, digital storage media for data storage and archiving, 10 and a means for control, acquisition, processing and display of results.

In a preferred embodiment, the cell screening system further comprises a 15 computer screen operatively associated with the computer for displaying data. In another preferred embodiment, the computer means for receiving and processing digital data from the digital camera stores the data in a bioinformatics data base. In a further preferred embodiment, the cell screening system further comprises a reader that measures a signal from many or all the wells in parallel. In another preferred 20 embodiment, the cell screening system further comprises a mechanical-optical means for changing the magnification of the system, to allow changing modes between high throughput and high content screening. In another preferred embodiment, the cell screening system further comprises a chamber and control system to maintain the temperature, CO₂ concentration and humidity surrounding the plate at levels required to 25 keep cells alive. In a further preferred embodiment, the cell screening system utilizes a confocal scanning illumination and detection system.

In another aspect of the present invention, a machine readable storage medium comprising a program containing a set of instructions for causing a cell screening system to execute procedures for defining the distribution and activity of specific 30 cellular constituents and processes is provided. In a preferred embodiment, the cell screening system comprises a high magnification fluorescence optical system with a stage adapted for holding cells and a means for moving the stage, a digital camera, a

light source for receiving and processing the digital data from the digital camera, and a computer means for receiving and processing the digital data from the digital camera. Preferred embodiments of the machine readable storage medium comprise programs consisting of a set of instructions for causing a cell screening system to execute the procedures set forth in Figures 9, 11, 12, 13, 14 or 15. Another preferred embodiment comprises a program consisting of a set of instructions for causing a cell screening system to execute procedures for detecting the distribution and activity of specific cellular constituents and processes. In most preferred embodiments, the cellular processes include, but are not limited to, nuclear translocation of a protein, cellular hypertrophy, apoptosis, and protease-induced translocation of a protein.

In another preferred embodiment, a variety of automated cell screening methods are provided, including screens to identify compounds that affect transcription factor activity, protein kinase activity, cell morphology, microtubule structure, apoptosis, receptor internalization, and protease-induced translocation of a protein.

15 In another aspect, the present invention provides recombinant nucleic acids encoding a protease biosensor, comprising:

- a. a first nucleic acid sequence that encodes at least one detectable polypeptide signal;
- b. a second nucleic acid sequence that encodes at least one protease recognition site, wherein the second nucleic acid sequence is operatively linked to the first nucleic acid sequence that encodes the at least one detectable polypeptide signal; and
- c. a third nucleic acid sequence that encodes at least one reactant target sequence, wherein the third nucleic acid sequence is operatively linked to the second nucleic acid sequence that encodes the at least one protease recognition site.

The present invention also provides the recombinant expression vectors capable of expressing the recombinant nucleic acids encoding protease biosensors, as well as genetically modified host cells that are transfected with the expression vectors.

30 The invention further provides recombinant protease biosensors, comprising

- a. a first domain comprising at least one detectable polypeptide signal;
- b. a second domain comprising at least one protease recognition site; and
- c. a third domain comprising at least one reactant target sequence;

wherein the first domain and the third domain are separated by the second domain.

In a further aspect, the present invention involves assays and reagents for characterizing a sample for the presence of a toxin. The method comprises the use of 5 detector, classifier, and identifier classes of toxin biosensors to provide for various levels of toxin characterization.

BRIEF DESCRIPTION OF THE DRAWINGS

- Figure 1** shows a diagram of the components of the cell-based scanning system.
10 **Figure 2** shows a schematic of the microscope subassembly.
Figure 3 shows the camera subassembly.
Figure 4 illustrates cell scanning system process.
Figure 5 illustrates a user interface showing major functions to guide the user.
15 **Figure 6** is a block diagram of the two platform architecture of the Dual Mode System for Cell Based Screening in which one platform uses a telescope lens to read all wells of a microtiter plate and a second platform that uses a higher magnification lens to read individual cells in a well.
20 **Figure 7** is a detail of an optical system for a single platform architecture of the Dual Mode System for Cell Based Screening that uses a moveable 'telescope' lens to read all wells of a microtiter plate and a moveable higher magnification lens to read individual cells in a well.
Figure 8 is an illustration of the fluid delivery system for acquiring kinetic data on the Cell Based Screening System.
25 **Figure 9** is a flow chart of processing step for the cell-based scanning system.
Figure 10 A-J illustrates the strategy of the Nuclear Translocation Assay.
Figure 11 is a flow chart defining the processing steps in the Dual Mode System for Cell Based Screening combining high throughput and high content screening of microtiter plates.
30 **Figure 12** is a flow chart defining the processing steps in the High Throughput mode of the System for Cell Based Screening.
Figure 13 is a flow chart defining the processing steps in the High Content mode of the System for Cell Based Screening.

Figure 14 is a flow chart defining the processing steps required for acquiring kinetic data in the High Content mode of the System for Cell Based Screening.

Figure 15 is a flow chart defining the processing steps performed within a well during the acquisition of kinetic data.

5 **Figure 16** is an example of data from a known inhibitor of translocation.

Figure 17 is an example of data from a known stimulator of translocation.

Figure 18 illustrates data presentation on a graphical display.

10 **Figure 19** is an illustration of the data from the High Throughput mode of the System for Cell Based Screening, an example of the data passed to the High Content mode, the data acquired in the high content mode, and the results of the analysis of that data,

Figure 20 shows the measurement of a drug-induced cytoplasm to nuclear translocation.

15 **Figure 21** illustrates a graphical user interface of the measurement shown in Figure 20.

Figure 22 illustrates a graphical user interface, with data presentation, of the measurement shown in Fig. 20.

20 **Figure 23** is a graph representing the kinetic data obtained from the measurements depicted in Fig. 20.

Figure 24 details a high-content screen of drug-induced apoptosis.

25 **Figure 25.** Graphs depicting changes in morphology upon induction of apoptosis.

20 Staurosporine (A) and paclitaxel (B) induce classic nuclear fragmentation in L929 cells. BHK cells exhibit concentration dependent changes in response to staurosporine (C), but a more classical response to paclitaxel (D). MCF-7 cells exhibit either nuclear condensation (E) or fragmentation (F) in response to staurosporine and paclitaxel, respectively. In all cases, cells were exposed to the compounds for 30 hours.

25 **Figure 26** illustrates the dose response of cells to staurosporine in terms of both nuclear size and nuclear perimeter convolution.

30 **Figure 27.** Graphs depicting induction of apoptosis by staurosporine and paclitaxel leading to changes in peri-nuclear f-actin content. (A, B) Both apoptotic stimulators induce dose-dependent increases in f-actin content in L929 cells. (C) In BHK cells, staurosporine induces a dose-dependent increase in f-actin, whereas paclitaxel (D) produces results that are more variable. (E) MCF-7 cells exhibit either a decrease or increase depending on the concentration of staurosporine. (F) Paclitaxel induced

changes in f-actin content were highly variable and not significant. Cells were exposed to the compounds for 30 hours.

Figure 28. Graphs depicting mitochondrial changes in response to induction of apoptosis. L929 (A,B) and BHK (C,D) cells responded to both staurosporine (A,C) and paclitaxel (B,D) with increases in mitochondrial mass. MCF-7 cells exhibit either a decrease in membrane potential (E, staurosporine) or an increase in mitochondrial mass (F, paclitaxel) depending on the stimulus. Cells were exposed to the compounds for 30 hours. 28G is a graph showing the simultaneous measurement of staurosporine effects on mitochondrial mass and mitochondrial potential in BHK cells.

10 Figure 29 shows the nucleic acid and amino acid sequence for various types of protease biosensor domains. (A) Signal sequences. (B) Protease recognition sites. (C) Product/Reactant target sequences

Figure 30 shows schematically shows some basic organization of domains in the protease biosensors of the invention.

15 Figure 31 is a schematic diagram of a specific 3-domain protease biosensor.

Figure 32 is a photograph showing the effect of stimulation of apoptosis by cis-platin on BHK cells transfected with an expression vector that expresses the caspase biosensor shown in Figure 32.

Figure 33 is a schematic diagram of a specific 4-domain protease biosensor.

20 Figure 34 is a schematic diagram of a specific 4-domain protease biosensor, containing a nucleolar localization signal.

Figure 35 is a schematic diagram of a specific 5-domain protease biosensor.

Figure 36 shows the differential response in a dual labeling assay of the p38 MAPK and NF- κ B pathways across three model toxins and two different cell types.

25 Treatments marked with an asterisk are different from controls at a 99% confidence level ($p < 0.01$).

DETAILED DESCRIPTION OF THE INVENTION

All cited patents, patent applications and other references are hereby
30 incorporated by reference in their entirety.

As used herein, the following terms have the specified meaning:

Markers of cellular domains. Luminescent probes that have high affinity for specific cellular constituents including specific organelles or molecules. These probes can either be small luminescent molecules or fluorescently tagged macromolecules used as "labeling reagents", "environmental indicators", or "biosensors."

5 *Labeling reagents.* Labeling reagents include, but are not limited to, luminescently labeled macromolecules including fluorescent protein analogs and biosensors, luminescent macromolecular chimeras including those formed with the green fluorescent protein and mutants thereof, luminescently labeled primary or secondary antibodies that react with cellular antigens involved in a physiological
10 response, luminescent stains, dyes, and other small molecules.

15 *Markers of cellular translocations.* Luminescently tagged macromolecules or organelles that move from one cell domain to another during some cellular process or physiological response. Translocation markers can either simply report location relative to the markers of cellular domains or they can also be "biosensors" that report some biochemical or molecular activity as well.

20 *Biosensors.* Macromolecules consisting of a biological functional domain and a luminescent probe or probes that report the environmental changes that occur either internally or on their surface. A class of luminescently labeled macromolecules designed to sense and report these changes have been termed "fluorescent-protein biosensors". The protein component of the biosensor provides a highly evolved molecular recognition moiety. A fluorescent molecule attached to the protein component in the proximity of an active site transduces environmental changes into fluorescence signals that are detected using a system with an appropriate temporal and spatial resolution such as the cell scanning system of the present invention. Because
25 the modulation of native protein activity within the living cell is reversible, and because fluorescent-protein biosensors can be designed to sense reversible changes in protein activity, these biosensors are essentially reusable.

30 *Disease associated sequences ("DAS").* This term refers to nucleic acid sequences identified by standard techniques, such as primary DNA sequence data, genomic methods such as subtraction hybridization and RAD_E, and proteomic methods in combination with reverse genetics, as being of drug candidate compounds. The term does not mean that the sequence is only associated with a disease state.

High content screening (HCS) can be used to measure the effects of drugs on complex molecular events such as signal transduction pathways, as well as cell functions including, but not limited to, apoptosis, cell division, cell adhesion, locomotion, exocytosis, and cell-cell communication. Multicolor fluorescence permits 5 multiple targets and cell processes to be assayed in a single screen. Cross-correlation of cellular responses will yield a wealth of information required for target validation and lead optimization.

In one aspect of the present invention, a cell screening system is provided comprising a high magnification fluorescence optical system having a microscope 10 objective, an XY stage adapted for holding a plate with an array of locations for holding cells and having a means for moving the plate to align the locations with the microscope objective and a means for moving the plate in the direction to effect focusing; a digital camera; a light source having optical means for directing excitation light to cells in the array of locations and a means for directing fluorescent light emitted 15 from the cells to the digital camera; and a computer means for receiving and processing digital data from the digital camera wherein the computer means includes: a digital frame grabber for receiving the images from the camera, a display for user interaction and display of assay results, digital storage media for data storage and archiving, and means for control, acquisition, processing and display of results.

20 Figure 1 is a schematic diagram of a preferred embodiment of the cell scanning system. An inverted fluorescence microscope is used 1, such as a Zeiss Axiovert inverted fluorescence microscope which uses standard objectives with magnification of 1-100x to the camera, and a white light source (e.g. 100W mercury-arc lamp or 75W xenon lamp) with power supply 2. There is an XY stage 3 to move the plate 4 in the 25 XY direction over the microscope objective. A Z-axis focus drive 5 moves the objective in the Z direction for focusing. A joystick 6 provides for manual movement of the stage in the XYZ direction. A high resolution digital camera 7 acquires images from each well or location on the plate. There is a camera power supply 8, an automation controller 9 and a central processing unit 10. The PC 11 provides a display 12 and has associated software. The printer 13 provides for printing of a hard copy record.

Figure 2 is a schematic of one embodiment of the microscope assembly 1 of the invention, showing in more detail the XY stage 3, Z-axis focus drive 5, joystick 6, light source 2, and automation controller 9. Cables to the computer 15 and microscope 16, respectively, are provided. In addition, Figure 2 shows a 96 well microtiter plate 17 which is moved on the XY stage 3 in the XY direction. Light from the light source 2 passes through the PC controlled shutter 18 to a motorized filter wheel 19 with excitation filters 20. The light passes into filter cube 25 which has a dichroic mirror 26 and an emission filter 27. Excitation light reflects off the dichroic mirror to the wells in the microtiter plate 17 and fluorescent light 28 passes through the dichroic mirror 26 and the emission filter 27 and to the digital camera 7.

Figure 3 shows a schematic drawing of a preferred camera assembly. The digital camera 7, which contains an automatic shutter for exposure control and a power supply 31, receives fluorescent light 28 from the microscope assembly. A digital cable 30 transports digital signals to the computer.

The standard optical configurations described above use microscope optics to directly produce an enlarged image of the specimen on the camera sensor in order to capture a high resolution image of the specimen. This optical system is commonly referred to as 'wide field' microscopy. Those skilled in the art of microscopy will recognize that a high resolution image of the specimen can be created by a variety of other optical systems, including, but not limited to, standard scanning confocal detection of a focused point or line of illumination scanned over the specimen (Go et al. 1997, *supra*), and multi-photon scanning confocal microscopy (Denk et al., 1990, *supra*), both of which can form images on a CCD detector or by synchronous digitization of the analog output of a photomultiplier tube.

In screening applications, it is often necessary to use a particular cell line, or primary cell culture, to take advantage of particular features of those cells. Those skilled in the art of cell culture will recognize that some cell lines are contact inhibited, meaning that they will stop growing when they become surrounded by other cells, while other cell lines will continue to grow under those conditions and the cells will literally pile up, forming many layers. An example of such a cell line is the HEK 293 (ATCC CRL-1573) line. An optical system that can acquire images of single cell layers in multilayer preparations is required for use with cell lines that tend to form

layers. The large depth of field of wide field microscopes produces an image that is a projection through the many layers of cells, making analysis of subcellular spatial distributions extremely difficult in layer-forming cells. Alternatively, the very shallow depth of field that can be achieved on a confocal microscope, (about one micron),
5 allows discrimination of a single cell layer at high resolution, simplifying the determination of the subcellular spatial distribution. Similarly, confocal imaging is preferable when detection modes such as fluorescence lifetime imaging are required.

The output of a standard confocal imaging attachment for a microscope is a digital image that can be converted to the same format as the images produced by the
10 other cell screening system embodiments described above, and can therefore be processed in exactly the same way as those images. The overall control, acquisition and analysis in this embodiment is essentially the same. The optical configuration of the confocal microscope system, is essentially the same as that described above, except for the illuminator and detectors. Illumination and detection systems required for
15 confocal microscopy have been designed as accessories to be attached to standard microscope optical systems such as that of the present invention (Zeiss, Germany). These alternative optical systems therefore can be easily integrated into the system as described above.

Figure 4 illustrates an alternative embodiment of the invention in which cell
20 arrays are in microwells 40 on a microplate 41, described in co-pending U.S. Application S/N 08/865,341, incorporated by reference herein in its entirety. Typically the microplate is 20 mm by 30 mm as compared to a standard 96 well microtiter plate which is 86 mm by 129 mm. The higher density array of cells on a microplate allows the microplate to be imaged at a low resolution of a few microns per pixel for high
25 throughput and particular locations on the microplate to be imaged at a higher resolution of less than 0.5 microns per pixel. These two resolution modes help to improve the overall throughput of the system.

The microplate chamber 42 serves as a microfluidic delivery system for the addition of compounds to cells. The microplate 41 in the microplate chamber 42 is
30 placed in an XY microplate reader 43. Digital data is processed as described above. The small size of this microplate system increases throughput, minimizes reagent volume and allows control of the distribution and placement of cells for fast and precise

cell-based analysis. Processed data can be displayed on a PC screen 11 and made part of a bioinformatics data base 44. This data base not only permits storage and retrieval of data obtained through the methods of this invention, but also permits acquisition and storage of external data relating to cells. Figure 5 is a PC display which illustrates the 5 operation of the software.

In an alternative embodiment, a high throughput system (HTS) is directly coupled with the HCS either on the same platform or on two separate platforms connected electronically (e.g. via a local area network). This embodiment of the 10 invention, referred to as a dual mode optical system, has the advantage of increasing the throughput of a HCS by coupling it with a HTS and thereby requiring slower high resolution data acquisition and analysis only on the small subset of wells that show a response in the coupled HTS.

High throughput 'whole plate' reader systems are well known in the art and are commonly used as a component of an HTS system used to screen large numbers of 15 compounds (Beggs (1997), *J. of Biomolec. Screening* 2:71-78; Macaffrey et al., (1996) *J. Biomolec. Screening* 1:187-190).

In one embodiment of dual mode cell based screening, a two platform architecture in which high throughput acquisition occurs on one platform and high content acquisition occurs on a second platform is provided (Figure 6). Processing 20 occurs on each platform independently, with results passed over a network interface, or a single controller is used to process the data from both platforms.

As illustrated in Figure 6, an exemplified two platform dual mode optical system consists of two light optical instruments, a high throughput platform 60 and a high content platform 65, which read fluorescent signals emitted from cells cultured in 25 microtiter plates or microwell arrays on a microplate, and communicate with each other via an electronic connection 64. The high throughput platform 60 analyzes all the wells in the whole plate either in parallel or rapid serial fashion. Those skilled in the art of screening will recognize that there are a many such commercially available high throughput reader systems that could be integrated into a dual mode cell based 30 screening system (Topcount (Packard Instruments, Meriden, CT); Spectramax, Lumiskan (Molecular Devices, Sunnyvale, CA); Fluoroscan (Labsystems, Beverly, MA)). The high content platform 65, as described above, scans from well to well and

acquires and analyzes high resolution image data collected from individual cells within a well.

The HTS software, residing on the system's computer 62, controls the high throughput instrument, and results are displayed on the monitor 61. The HCS software, residing on it's computer system 67, controls the high content instrument hardware 65, optional devices (e.g. plate loader, environmental chamber, fluid dispenser), analyzes digital image data from the plate, displays results on the monitor 66 and manages data measured in an integrated database. The two systems can also share a single computer, in which case all data would be collected, processed and displayed on that computer, without the need for a local area network to transfer the data. Microtiter plates are transferred from the high throughput system to the high content system 63 either manually or by a robotic plate transfer device, as is well known in the art (Beggs (1997), *supra*; Mcaffrey (1996), *supra*).

In a preferred embodiment, the dual mode optical system utilizes a single platform system (Figure 7). It consists of two separate optical modules, an HCS module 203 and an HTS module 209 that can be independently or collectively moved so that only one at a time is used to collect data from the microtiter plate 201. The microtiter plate 201 is mounted in a motorized X,Y stage so it can be positioned for imaging in either HTS or HCS mode. After collecting and analyzing the HTS image data as described below, the HTS optical module 209 is moved out of the optical path and the HCS optical module 203 is moved into place.

The optical module for HTS 209 consists of a projection lens 214, excitation wavelength filter 213 and dichroic mirror 210 which are used to illuminate the whole bottom of the plate with a specific wavelength band from a conventional microscope lamp system (not illustrated). The fluorescence emission is collected through the dichroic mirror 210 and emission wavelength filter 211 by a lens 212 which forms an image on the camera 216 with sensor 215.

The optical module for HCS 203 consists of a projection lens 208, excitation wavelength filter 207 and dichroic mirror 204 which are used to illuminate the back aperture of the microscope objective 202, and thereby the field of that objective, from a standard microscope illumination system (not shown). The fluorescence emission is

collected by the microscope objective 202, passes through the dichroic mirror 204 and emission wavelength filter 205 and is focused by a tube lens 206 which forms an image on the same camera 216 with sensor 215.

In an alternative embodiment of the present invention, the cell screening system
5 further comprises a fluid delivery device for use with the live cell embodiment of the method of cell screening (see below). Figure 8 exemplifies a fluid delivery device for use with the system of the invention. It consists of a bank of 12 syringe pumps 701 driven by a single motor drive. Each syringe 702 is sized according to the volume to be delivered to each well, typically between 1 and 100 μ L. Each syringe is attached via
10 flexible tubing 703 to a similar bank of connectors which accept standard pipette tips 705. The bank of pipette tips are attached to a drive system so they can be lowered and raised relative to the microtiter plate 706 to deliver fluid to each well. The plate is mounted on an X,Y stage, allowing movement relative to the optical system 707 for data collection purposes. This set-up allows one set of pipette tips, or even a single
15 pipette tip, to deliver reagent to all the wells on the plate. The bank of syringe pumps can be used to deliver fluid to 12 wells simultaneously, or to fewer wells by removing some of the tips.

In another aspect, the present invention provides a method for analyzing cells comprising providing an array of locations which contain multiple cells wherein the
20 cells contain one or more fluorescent reporter molecules; scanning multiple cells in each of the locations containing cells to obtain fluorescent signals from the fluorescent reporter molecule in the cells; converting the fluorescent signals into digital data; and utilizing the digital data to determine the distribution, environment or activity of the fluorescent reporter molecule within the cells.

25

Cell Arrays

Screening large numbers of compounds for activity with respect to a particular biological function requires preparing arrays of cells for parallel handling of cells and reagents. Standard 96 well microtiter plates which are 86 mm by 129 mm, with 6mm
30 diameter wells on a 9mm pitch, are used for compatibility with current automated loading and robotic handling systems. The microplate is typically 20 mm by 30 mm, with cell locations that are 100-200 microns in dimension on a pitch of about 500

microns. Methods for making microplates are described in U.S. Patent Application Serial No. 08/865,341, incorporated by reference herein in its entirety. Microplates may consist of coplanar layers of materials to which cells adhere, patterned with materials to which cells will not adhere, or etched 3-dimensional surfaces of similarly pattered materials. For the purpose of the following discussion, the terms 'well' and 'microwell' refer to a location in an array of any construction to which cells adhere and within which the cells are imaged. Microplates may also include fluid delivery channels in the spaces between the wells. The smaller format of a microplate increases the overall efficiency of the system by minimizing the quantities of the reagents, storage and handling during preparation and the overall movement required for the scanning operation. In addition, the whole area of the microplate can be imaged more efficiently, allowing a second mode of operation for the microplate reader as described later in this document.

Fluorescence Reporter Molecules

A major component of the new drug discovery paradigm is a continually growing family of fluorescent and luminescent reagents that are used to measure the temporal and spatial distribution, content, and activity of intracellular ions, metabolites, macromolecules, and organelles. Classes of these reagents include labeling reagents that measure the distribution and amount of molecules in living and fixed cells, environmental indicators to report signal transduction events in time and space, and fluorescent protein biosensors to measure target molecular activities within living cells. A multiparameter approach that combines several reagents in a single cell is a powerful new tool for drug discovery.

The method of the present invention is based on the high affinity of fluorescent or luminescent molecules for specific cellular components. The affinity for specific components is governed by physical forces such as ionic interactions, covalent bonding (which includes chimeric fusion with protein-based chromophores, fluorophores, and lumiphores), as well as hydrophobic interactions, electrical potential, and, in some cases, simple entrapment within a cellular component. The luminescent probes can be small molecules, labeled macromolecules, or genetically engineered proteins, including, but not limited to green fluorescent protein chimeras.

Those skilled in this art will recognize a wide variety of fluorescent reporter molecules that can be used in the present invention, including, but not limited to, fluorescently labeled biomolecules such as proteins, phospholipids and DNA hybridizing probes. Similarly, fluorescent reagents specifically synthesized with particular chemical properties of binding or association have been used as fluorescent reporter molecules (Barak et al., (1997), *J. Biol. Chem.* 272:27497-27500; Southwick et al., (1990), *Cytometry* 11:418-430; Tsien (1989) in *Methods in Cell Biology*, Vol. 29 Taylor and Wang (eds.), pp. 127-156). Fluorescently labeled antibodies are particularly useful reporter molecules due to their high degree of specificity for attaching to a single molecular target in a mixture of molecules as complex as a cell or tissue.

The luminescent probes can be synthesized within the living cell or can be transported into the cell via several non-mechanical modes including diffusion, facilitated or active transport, signal-sequence-mediated transport, and endocytotic or pinocytotic uptake. Mechanical bulk loading methods, which are well known in the art, can also be used to load luminescent probes into living cells (Barber et al. (1996), *Neuroscience Letters* 207:17-20; Bright et al. (1996), *Cytometry* 24:226-233; McNeil (1989) in *Methods in Cell Biology*, Vol. 29, Taylor and Wang (eds.), pp. 153-173). These methods include electroporation and other mechanical methods such as scrape-loading, bead-loading, impact-loading, syringe-loading, hypertonic and hypotonic loading. Additionally, cells can be genetically engineered to express reporter molecules, such as GFP, coupled to a protein of interest as previously described (Chalfie and Prasher U.S. Patent No. 5,491,084; Cubitt et al. (1995), *Trends in Biochemical Science* 20:448-455).

Once in the cell, the luminescent probes accumulate at their target domain as a result of specific and high affinity interactions with the target domain or other modes of molecular targeting such as signal-sequence-mediated transport. Fluorescently labeled reporter molecules are useful for determining the location, amount and chemical environment of the reporter. For example, whether the reporter is in a lipophilic membrane environment or in a more aqueous environment can be determined (Giuliano et al. (1995), *Ann. Rev. of Biophysics and Biomolecular Structure* 24:405-434; Giuliano and Taylor (1995), *Methods in Neuroscience* 27:1-16). The pH environment of the reporter can be determined (Bright et al. (1989), *J. Cell Biology* 104:1019-1033;

Giuliano et al. (1987), *Anal. Biochem.* 167:362-371; Thomas et al. (1979), *Biochemistry* 18:2210-2218). It can be determined whether a reporter having a chelating group is bound to an ion, such as Ca⁺⁺, or not (Bright et al. (1989), In *Methods in Cell Biology*, Vol. 30, Taylor and Wang (eds.), pp. 157-192; Shimoura et al. 5 (1988), *J. of Biochemistry* (Tokyo) 251:405-410; Tsien (1989) In *Methods in Cell Biology*, Vol. 30, Taylor and Wang (eds.), pp. 127-156).

Furthermore, certain cell types within an organism may contain components that can be specifically labeled that may not occur in other cell types. For example, epithelial cells often contain polarized membrane components. That is, these cells 10 asymmetrically distribute macromolecules along their plasma membrane. Connective or supporting tissue cells often contain granules in which are trapped molecules specific to that cell type (e.g., heparin, histamine, serotonin, etc.). Most muscular tissue cells contain a sarcoplasmic reticulum, a specialized organelle whose function is to regulate the concentration of calcium ions within the cell cytoplasm. Many nervous tissue cells 15 contain secretory granules and vesicles in which are trapped neurohormones or neurotransmitters. Therefore, fluorescent molecules can be designed to label not only specific components within specific cells, but also specific cells within a population of mixed cell types.

Those skilled in the art will recognize a wide variety of ways to measure 20 fluorescence. For example, some fluorescent reporter molecules exhibit a change in excitation or emission spectra, some exhibit resonance energy transfer where one fluorescent reporter loses fluorescence, while a second gains in fluorescence, some exhibit a loss (quenching) or appearance of fluorescence, while some report rotational movements (Giuliano et al. (1995), *Ann. Rev. of Biophysics and Biomol. Structure* 25 24:405-434; Giuliano et al. (1995), *Methods in Neuroscience* 27:1-16).

Scanning cell arrays

Referring to Figure 9, a preferred embodiment is provided to analyze cells that comprises operator-directed parameters being selected based on the assay being conducted, data acquisition by the cell screening system on the distribution of 30 fluorescent signals within a sample, and interactive data review and analysis. At the start of an automated scan the operator enters information 100 that describes the sample, specifies the filter settings and fluorescent channels to match the biological

labels being used and the information sought, and then adjusts the camera settings to match the sample brightness. For flexibility to handle a range of samples, the software allows selection of various parameter settings used to identify nuclei and cytoplasm, and selection of different fluorescent reagents, identification of cells of interest based
5 on morphology or brightness, and cell numbers to be analyzed per well. These parameters are stored in the system's for easy retrieval for each automated run. The system's interactive cell identification mode simplifies the selection of morphological parameter limits such as the range of size, shape, and intensity of cells to be analyzed. The user specifies which wells of the plate the system will scan and how many fields or
10 how many cells to analyze in each well. Depending on the setup mode selected by the user at step 101, the system either automatically pre-focuses the region of the plate to be scanned using an autofocus procedure to "find focus" of the plate 102 or the user interactively pre-focuses 103 the scanning region by selecting three "tag" points which define the rectangular area to be scanned. A least-squares fit "focal plane model" is
15 then calculated from these tag points to estimate the focus of each well during an automated scan. The focus of each well is estimated by interpolating from the focal plane model during a scan.

During an automated scan, the software dynamically displays the scan status, including the number of cells analyzed, the current well being analyzed, images of each
20 independent wavelength as they are acquired, and the result of the screen for each well as it is determined. The plate 4 (Figure 1) is scanned in a serpentine style as the software automatically moves the motorized microscope XY stage 3 from well to well and field to field within each well of a 96-well plate. Those skilled in the programming art will recognize how to adapt software for scanning of other microplate formats such
25 as 24, 48, and 384 well plates. The scan pattern of the entire plate as well as the scan pattern of fields within each well are programmed. The system adjusts sample focus with an autofocus procedure 104 (Figure 9) through the Z axis focus drive 5, controls filter selection via a motorized filter wheel 19, and acquires and analyzes images of up to four different colors ("channels" or "wavelengths").

30 The autofocus procedure is called at a user selected frequency, typically for the first field in each well and then once every 4 to 5 fields within each well. The autofocus procedure calculates the starting Z-axis point by interpolating from the pre-calculated

plane focal model. Starting a programmable distance above or below this set point, the procedure moves the mechanical Z-axis through a number of different positions, acquires an image at each position, and finds the maximum of a calculated focus score that estimates the contrast of each image. The Z position of the image with the 5 maximum focus score determines the best focus for a particular field. Those skilled in the art will recognize this as a variant of automatic focusing methods as described in Harms et al. in *Cytometry* 5 (1984), 236-243, Groen et al. in *Cytometry* 6 (1985), 81-91, and Firestone et al. in *Cytometry* 12 (1991), 195-206.

For image acquisition, the camera's exposure time is separately adjusted for 10 each dye to ensure a high-quality image from each channel. Software procedures can be called, at the user's option, to correct for registration shifts between wavelengths by accounting for linear (X and Y) shifts between wavelengths before making any further measurements. The electronic shutter 18 is controlled so that sample photo-bleaching is kept to a minimum. Background shading and uneven illumination can be corrected by 15 the software using methods known in the art (Bright et al. (1987), *J. Cell Biol.* 104:1019-1033).

In one channel, images are acquired of a primary marker 105 (Figure 9) (typically cell nuclei counterstained with DAPI or PI fluorescent dyes) which are 20 segmented ("identified") using an adaptive thresholding procedure. The adaptive thresholding procedure 106 is used to dynamically select the threshold of an image for separating cells from the background. The staining of cells with fluorescent dyes can vary to an unknown degree across cells in a microtiter plate sample as well as within images of a field of cells within each well of a microtiter plate. This variation can occur as a result of sample preparation and/or the dynamic nature of cells. A global threshold 25 is calculated for the complete image to separate the cells from background and account for field to field variation. These global adaptive techniques are variants of those described in the art. (Kittler et al. in *Computer Vision, Graphics, and Image Processing* 30 (1985), 125-147, Ridler et al. in *IEEE Trans. Systems, Man, and Cybernetics* (1978), 630-632.)

30 An alternative adaptive thresholding method utilizes local region thresholding in contrast to global image thresholding. Image analysis of local regions leads to better overall segmentation since staining of cell nuclei (as well as other labeled components)

can vary across an image. Using this global/local procedure, a reduced resolution image (reduced in size by a factor of 2 to 4) is first globally segmented (using adaptive thresholding) to find regions of interest in the image. These regions then serve as guides to more fully analyze the same regions at full resolution. A more localized 5 threshold is then calculated (again using adaptive thresholding) for each region of interest.

The output of the segmentation procedure is a binary image wherein the objects are white and the background is black. This binary image, also called a mask in the art, is used to determine if the field contains objects 107. The mask is labeled with a blob 10 labeling method whereby each object (or blob) has a unique number assigned to it. Morphological features, such as area and shape, of the blobs are used to differentiate blobs likely to be cells from those that are considered artifacts. The user pre-sets the morphological selection criteria by either typing in known cell morphological features or by using the interactive training utility. If objects of interest are found in the field, 15 images are acquired for all other active channels 108, otherwise the stage is advanced to the next field 109 in the current well. Each object of interest is located in the image for further analysis 110. The software determines if the object meets the criteria for a valid cell nucleus 111 by measuring its morphological features (size and shape). For each valid cell, the XYZ stage location is recorded, a small image of the cell is stored, 20 and features are measured 112.

The cell scanning method of the present invention can be used to perform many different assays on cellular samples by applying a number of analytical methods simultaneously to measure features at multiple wavelengths. An example of one such assay provides for the following measurements:

- 25 1. The total fluorescent intensity within the cell nucleus for colors 1-4
2. The area of the cell nucleus for color 1 (the primary marker)
3. The shape of the cell nucleus for color 1 is described by three shape features:
 - 30 a) perimeter squared area
 - b) box area ratio
 - c) height width ratio
4. The average fluorescent intensity within the cell nucleus for colors 1-4 (i.e. #1 divided by #2)
- 35 5. The total fluorescent intensity of a ring outside the nucleus (see Figure 10) that represents fluorescence of the cell's cytoplasm (cytoplasmic mask) for colors 2-4

6. The area of the cytoplasmic mask
7. The average fluorescent intensity of the cytoplasmic mask for colors 2-4 (i.e. #5 divided by #6)
8. The ratio of the average fluorescent intensity of the cytoplasmic mask to average fluorescent intensity within the cell nucleus for colors 2-4 (i.e. #7 divided by #4)
9. The difference of the average fluorescent intensity of the cytoplasmic mask and the average fluorescent intensity within the cell nucleus for colors 2-4 (i.e. #7 minus #4)
10. 10. The number of fluorescent domains (also call spots, dots, or grains) within the cell nucleus for colors 2-4

Features 1 through 4 are general features of the different cell screening assays of the invention. These steps are commonly used in a variety of image analysis applications and are well known in art (Russ (1992) *The Image Processing Handbook*, CRC Press Inc.; Gonzales et al. (1987), *Digital Image Processing*. Addison-Wesley Publishing Co. pp. 391-448). Features 5-9 have been developed specifically to provide measurements of a cell's fluorescent molecules within the local cytoplasmic region of the cell and the translocation (i.e. movement) of fluorescent molecules from the cytoplasm to the nucleus. These features (steps 5-9) are used for analyzing cells in microplates for the inhibition of nuclear translocation. For example, inhibition of nuclear translocation of transcription factors provides a novel approach to screening intact cells (detailed examples of other types of screens will be provided below). A specific method measures the amount of probe in the nuclear region (feature 4) versus the local cytoplasmic region (feature 7) of each cell. Quantification of the difference between these two sub-cellular compartments provides a measure of cytoplasm-nuclear translocation (feature 9).

Feature 10 describes a screen used for counting of DNA or RNA probes within the nuclear region in colors 2-4. For example, probes are commercially available for identifying chromosome-specific DNA sequences (Life Technologies, Gaithersburg, MD; Genosys, Woodlands, TX; Biotechnologies, Inc., Richmond, CA; Bio 101, Inc., Vista, CA) Cells are three-dimensional in nature and when examined at a high magnification under a microscope one probe may be in-focus while another may be completely out-of-focus. The cell screening method of the present invention provides for detecting three-dimensional probes in nuclei by acquiring images from multiple focal planes. The software moves the Z-axis motor drive 5 (Figure 1) in small steps

where the step distance is user selected to account for a wide range of different nuclear diameters. At each of the focal steps, an image is acquired. The maximum gray-level intensity from each pixel in each image is found and stored in a resulting maximum projection image. The maximum projection image is then used to count the probes. The 5 above method works well in counting probes that are not stacked directly above or below another one. To account for probes stacked on top of each other in the Z-direction, users can select an option to analyze probes in each of the focal planes acquired. In this mode, the scanning system performs the maximum plane projection method as discussed above, detects probe regions of interest in this image, then further 10 analyzes these regions in all the focal plane images.

After measuring cell features 112 (Figure 9), the system checks if there are any unprocessed objects in the current field 113. If there are any unprocessed objects, it locates the next object 110 and determines whether it meets the criteria for a valid cell nucleus 111, and measures its features. Once all the objects in the current field are 15 processed, the system determines whether analysis of the current plate is complete 114; if not, it determines the need to find more cells in the current well 115. If the need exists, the system advances the XYZ stage to the next field within the current well 109 or advances the stage to the next well 116 of the plate.

After a plate scan is complete, images and data can be reviewed with the 20 system's image review, data review, and summary review facilities. All images, data, and settings from a scan are archived in the system's database for later review or for interfacing with a network information management system. Data can also be exported to other third-party statistical packages to tabulate results and generate other reports. Users can review the images alone of every cell analyzed by the system with an 25 interactive image review procedure 117. The user can review data on a cell-by-cell basis using a combination of interactive graphs, a data spreadsheet of measured features, and images of all the fluorescence channels of a cell of interest with the interactive cell-by-cell data review procedure 118. Graphical plotting capabilities are provided in which data can be analyzed via interactive graphs such as histograms and 30 scatter plots. Users can review summary data that are accumulated and summarized for all cells within each well of a plate with an interactive well-by-well data review

procedure 119. Hard copies of graphs and images can be printed on a wide range of standard printers.

As a final phase of a complete scan, reports can be generated on one or more statistics of the measured features. Users can generate a graphical report of data 5 summarized on a well-by-well basis for the scanned region of the plate using an interactive report generation procedure 120. This report includes a summary of the statistics by well in tabular and graphical format and identification information on the sample. The report window allows the operator to enter comments about the scan for later retrieval. Multiple reports can be generated on many statistics and be printed with 10 the touch of one button. Reports can be previewed for placement and data before being printed.

The above-recited embodiment of the method operates in a single high resolution mode referred to as the high content screening (HCS) mode. The HCS mode provides sufficient spatial resolution within a well (on the order of 1 μm) to define the 15 distribution of material within the well, as well as within individual cells in the well. The high degree of information content accessible in that mode, comes at the expense of speed and complexity of the required signal processing.

In an alternative embodiment, a high throughput system (HTS) is directly coupled with the HCS either on the same platform or on two separate platforms 20 connected electronically (e.g. via a local area network). This embodiment of the invention, referred to as a dual mode optical system, has the advantage of increasing the throughput of an HCS by coupling it with an HTS and thereby requiring slower high resolution data acquisition and analysis only on the small subset of wells that show a response in the coupled HTS.

25 High throughput 'whole plate' reader systems are well known in the art and are commonly used as a component of an HTS system used to screen large numbers of compounds (Beggs et al. (1997), *supra*; McCaffrey et al. (1996), *supra*). The HTS of the present invention is carried out on the microtiter plate or microwell array by reading many or all wells in the plate simultaneously with sufficient resolution to make 30 determinations on a well-by-well basis. That is, calculations are made by averaging the total signal output of many or all the cells or the bulk of the material in each well.

Wells that exhibit some defined response in the HTS (the 'hits') are flagged by the system. Then on the same microtiter plate or microwell array, each well identified as a hit is measured via HCS as described above. Thus, the dual mode process involves:

1. Rapidly measuring numerous wells of a microtiter plate or microwell array,
- 5 2. Interpreting the data to determine the overall activity of fluorescently labeled reporter molecules in the cells on a well-by-well basis to identify "hits" (wells that exhibit a defined response),
3. Imaging numerous cells in each "hit" well, and
- 10 4. Interpreting the digital image data to determine the distribution, environment or activity of the fluorescently labeled reporter molecules in the individual cells (i.e. intracellular measurements) and the distribution of the cells to test for specific biological functions

In a preferred embodiment of dual mode processing (Figure 11), at the start of a run 301, the operator enters information 302 that describes the plate and its contents, specifies the filter settings and fluorescent channels to match the biological labels being used, the information sought and the camera settings to match the sample brightness. These parameters are stored in the system's database for easy retrieval for each automated run. The microtiter plate or microwell array is loaded into the cell screening system 303 either manually or automatically by controlling a robotic loading device. An optional environmental chamber 304 is controlled by the system to maintain the temperature, humidity and CO₂ levels in the air surrounding live cells in the microtiter plate or microwell array. An optional fluid delivery device 305 (see Figure 8) is controlled by the system to dispense fluids into the wells during the scan.

25 High throughput processing 306 is first performed on the microtiter plate or microwell array by acquiring and analyzing the signal from each of the wells in the plate. The processing performed in high throughput mode 307 is illustrated in Figure 12 and described below. Wells that exhibit some selected intensity response in this high throughput mode ("hits") are identified by the system. The system performs a conditional operation 308 that tests for hits. If hits are found, those specific hit wells are further analyzed in high content (micro level) mode 309. The processing performed in high content mode 312 is illustrated in Figure 13. The system then updates 310 the informatics database 311 with results of the measurements on the plate. If there are

more plates to be analyzed 313 the system loads the next plate 303; otherwise the analysis of the plates terminates 314.

The following discussion describes the high throughput mode illustrated in Figure 12. The preferred embodiment of the system, the single platform dual mode screening system, will be described. Those skilled in the art will recognize that operationally the dual platform system simply involves moving the plate between two optical systems rather than moving the optics. Once the system has been set up and the plate loaded, the system begins the HTS acquisition and analysis 401. The HTS optical module is selected by controlling a motorized optical positioning device 402 on the dual mode system. In one fluorescence channel, data from a primary marker on the plate is acquired 403 and wells are isolated from the plate background using a masking procedure 404. Images are also acquired in other fluorescence channels being used 405. The region in each image corresponding to each well 406 is measured 407. A feature calculated from the measurements for a particular well is compared with a predefined threshold or intensity response 408, and based on the result the well is either flagged as a "hit" 409 or not. The locations of the wells flagged as hits are recorded for subsequent high content mode processing. If there are wells remaining to be processed 410 the program loops back 406 until all the wells have been processed 411 and the system exits high throughput mode.

Following HTS analysis, the system starts the high content mode processing 501 defined in Figure 13. The system selects the HCS optical module 502 by controlling the motorized positioning system. For each "hit" well identified in high throughput mode, the XY stage location of the well is retrieved from memory or disk and the stage is then moved to the selected stage location 503. The autofocus procedure 504 is called for the first field in each hit well and then once every 5 to 8 fields within each well. In one channel, images are acquired of the primary marker 505 (typically cell nuclei counterstained with DAPI, Hoechst or PI fluorescent dye). The images are then segmented (separated into regions of nuclei and non-nuclei) using an adaptive thresholding procedure 506. The output of the segmentation procedure is a binary mask wherein the objects are white and the background is black. This binary image, also called a mask in the art, is used to determine if the field contains objects 507. The mask

is labeled with a blob labeling method whereby each object (or blob) has a unique number assigned to it. If objects are found in the field, images are acquired for all other active channels 508, otherwise the stage is advanced to the next field 514 in the current well. Each object is located in the image for further analysis 509. Morphological features, such as area and shape of the objects, are used to select objects likely to be cell nuclei 510, and discard (do no further processing on) those that are considered artifacts. For each valid cell nucleus, the XYZ stage location is recorded, a small image of the cell is stored, and assay specific features are measured 511. The system then performs multiple tests on the cells by applying several analytical methods to measure features at each of several wavelengths. After measuring the cell features, the systems checks if there are any unprocessed objects in the current field 512. If there are any unprocessed objects, it locates the next object 509 and determines whether it meets the criteria for a valid cell nucleus 510, and measures its features. After processing all the objects in the current field, the system determines whether it needs to find more cells or fields in the current well 513. If it needs to find more cells or fields in the current well it advances the XYZ stage to the next field within the current well 515. Otherwise, the system checks whether it has any remaining hit wells to measure 515. If so, it advances to the next hit well 503 and proceeds through another cycle of acquisition and analysis, otherwise the HCS mode is finished 516.

In an alternative embodiment of the present invention, a method of kinetic live cell screening is provided. The previously described embodiments of the invention are used to characterize the spatial distribution of cellular components at a specific point in time, the time of chemical fixation. As such, these embodiments have limited utility for implementing kinetic based screens, due to the sequential nature of the image acquisition, and the amount of time required to read all the wells on a plate. For example, since a plate can require 30 – 60 minutes to read through all the wells, only very slow kinetic processes can be measured by simply preparing a plate of live cells and then reading through all the wells more than once. Faster kinetic processes can be measured by taking multiple readings of each well before proceeding to the next well, but the elapsed time between the first and last well would be too long, and fast kinetic processes would likely be complete before reaching the last well.

The kinetic live cell extension of the invention enables the design and use of screens in which a biological process is characterized by its kinetics instead of, or in addition to, its spatial characteristics. In many cases, a response in live cells can be measured by adding a reagent to a specific well and making multiple measurements on 5 that well with the appropriate timing. This dynamic live cell embodiment of the invention therefore includes apparatus for fluid delivery to individual wells of the system in order to deliver reagents to each well at a specific time in advance of reading the well. This embodiment thereby allows kinetic measurements to be made with temporal resolution of seconds to minutes on each well of the plate. To improve the 10 overall efficiency of the dynamic live cell system, the acquisition control program is modified to allow repetitive data collection from sub-regions of the plate, allowing the system to read other wells between the time points required for an individual well.

Figure 8 describes an example of a fluid delivery device for use with the live cell embodiment of the invention and is described above. This set-up allows one set of 15 pipette tips 705, or even a single pipette tip, to deliver reagent to all the wells on the plate. The bank of syringe pumps 701 can be used to deliver fluid to 12 wells simultaneously, or to fewer wells by removing some of the tips 705. The temporal resolution of the system can therefore be adjusted, without sacrificing data collection efficiency, by changing the number of tips and the scan pattern as follows. Typically, 20 the data collection and analysis from a single well takes about 5 seconds. Moving from well to well and focusing in a well requires about 5 seconds, so the overall cycle time for a well is about 10 seconds. Therefore, if a single pipette tip is used to deliver fluid to a single well, and data is collected repetitively from that well, measurements can be made with about 5 seconds temporal resolution. If 6 pipette tips are used to deliver 25 fluids to 6 wells simultaneously, and the system repetitively scans all 6 wells, each scan will require 60 seconds, thereby establishing the temporal resolution. For slower processes which only require data collection every 8 minutes, fluids can be delivered to one half of the plate, by moving the plate during the fluid delivery phase, and then repetitively scanning that half of the plate. Therefore, by adjusting the size of the sub-region being scanned on the plate, the temporal resolution can be adjusted without 30 having to insert wait times between acquisitions. Because the system is continuously scanning and acquiring data, the overall time to collect a kinetic data set from the plate

is then simply the time to perform a single scan of the plate, multiplied by the number of time points required. Typically, 1 time point before addition of compounds and 2 or 3 time points following addition should be sufficient for screening purposes.

Figure 14 shows the acquisition sequence used for kinetic analysis. The start of processing 801 is configuration of the system, much of which is identical to the standard HCS configuration. In addition, the operator must enter information specific to the kinetic analysis being performed 802, such as the sub-region size, the number of time points required, and the required time increment. A sub-region is a group of wells that will be scanned repetitively in order to accumulate kinetic data. The size of the sub-region is adjusted so that the system can scan a whole sub-region once during a single time increment, thus minimizing wait times. The optimum sub-region size is calculated from the setup parameters, and adjusted if necessary by the operator. The system then moves the plate to the first sub-region 803, and to the first well in that sub-region 804 to acquire the prestimulation (time = 0) time points. The acquisition sequence performed in each well is exactly the same as that required for the specific HCS being run in kinetic mode. Figure 15 details a flow chart for that processing. All of the steps between the start 901 and the return 902 are identical to those described as steps 504 – 514 in Figure 13.

After processing each well in a sub-region, the system checks to see if all the wells in the sub-region have been processed 806 (Figure 14), and cycles through all the wells until the whole region has been processed. The system then moves the plate into position for fluid addition, and controls fluidic system delivery of fluids to the entire sub-region 807. This may require multiple additions for sub-regions which span several rows on the plate, with the system moving the plate on the X,Y stage between additions. Once the fluids have been added, the system moves to the first well in the sub-region 808 to begin acquisition of time points. The data is acquired from each well 809 and as before the system cycles through all the wells in the sub-region 810. After each pass through the sub-region, the system checks whether all the time points have been collected 811 and if not, pauses 813 if necessary 812 to stay synchronized with the requested time increment. Otherwise, the system checks for additional sub-regions on the plate 814 and either moves to the next sub-region 803 or finishes 815. Thus, the

kinetic analysis mode comprises operator identification of sub-regions of the microtiter plate or microwells to be screened, based on the kinetic response to be investigated, with data acquisitions within a sub-region prior to data acquisition in subsequent sub-regions.

5 *Specific Screens*

In another aspect of the present invention, cell screening methods and machine readable storage medium comprising a program containing a set of instructions for causing a cell screening system to execute procedures for defining the distribution and activity of specific cellular constituents and processes is provided. In a preferred 10 embodiment, the cell screening system comprises a high magnification fluorescence optical system with a stage adapted for holding cells and a means for moving the stage, a digital camera, a light source for receiving and processing the digital data from the digital camera, and a computer means for receiving and processing the digital data from the digital camera. This aspect of the invention comprises programs that instruct the 15 cell screening system to define the distribution and activity of specific cellular constituents and processes, using the luminescent probes, the optical imaging system, and the pattern recognition software of the invention. Preferred embodiments of the machine readable storage medium comprise programs consisting of a set of instructions for causing a cell screening system to execute the procedures set forth in Figures 9, 11, 20 12, 13, 14 or 15. Another preferred embodiment comprises a program consisting of a set of instructions for causing a cell screening system to execute procedures for detecting the distribution and activity of specific cellular constituents and processes. In most preferred embodiments, the cellular processes include, but are not limited to, nuclear translocation of a protein, cellular morphology, apoptosis, receptor 25 internalization, and protease-induced translocation of a protein.

In a preferred embodiment, the cell screening methods are used to identify compounds that modify the various cellular processes. The cells can be contacted with a test compound, and the effect of the test compound on a particular cellular process can be analyzed. Alternatively, the cells can be contacted with a test compound and a 30 known agent that modifies the particular cellular process, to determine whether the test compound can inhibit or enhance the effect of the known agent. Thus, the methods can

be used to identify test compounds that increase or decrease a particular cellular response, as well as to identify test compounds that affects the ability of other agents to increase or decrease a particular cellular response.

In another preferred embodiment, the locations containing cells are analyzed
5 using the above methods at low resolution in a high throughput mode, and only a subset
of the locations containing cells are analyzed in a high content mode to obtain
luminescent signals from the luminescently labeled reporter molecules in subcellular
compartments of the cells being analyzed.

The following examples are intended for purposes of illustration only and
10 should not be construed to limit the scope of the invention, as defined in the claims
appended hereto.

The various chemical compounds, reagents, dyes, and antibodies that are
referred to in the following Examples are commercially available from such sources as
Sigma Chemical (St. Louis, MO), Molecular Probes (Eugene, OR), Aldrich Chemical
15 Company (Milwaukee, WI), Accurate Chemical Company (Westbury, NY), Jackson
Immunolabs, and Clontech (Palo Alto, CA).

Example 1 Cytoplasm to Nucleus Translocation Screening:

a. Transcription Factors

Regulation of transcription of some genes involves activation of a transcription
factor in the cytoplasm, resulting in that factor being transported into the nucleus where
it can initiate transcription of a particular gene or genes. This change in transcription
factor distribution is the basis of a screen for the cell-based screening system to detect
compounds that inhibit or induce transcription of a particular gene or group of genes.
25 A general description of the screen is given followed by a specific example.

The distribution of the transcription factor is determined by labeling the nuclei
with a DNA specific fluorophore like Hoechst 33423 and the transcription factor with a
specific fluorescent antibody. After autofocusing on the Hoechst labeled nuclei, an
image of the nuclei is acquired in the cell-based screening system and used to create a
30 mask by one of several optional thresholding methods, as described *supra*. The
morphological descriptors of the regions defined by the mask are compared with the

user defined parameters and valid nuclear masks are identified and used with the following method to extract transcription factor distributions. Each valid nuclear mask is eroded to define a slightly smaller nuclear region. The original nuclear mask is then dilated in two steps to define a ring shaped region around the nucleus, which represents a cytoplasmic region. The average antibody fluorescence in each of these two regions is determined, and the difference between these averages is defined as the NucCyt Difference. Two examples of determining nuclear translocation are discussed below and illustrated in Figure 10A-J. Figure 10A illustrates an unstimulated cell with its nucleus 200 labeled with a blue fluorophore and a transcription factor in the cytoplasm 201 labeled with a green fluorophore. Figure 10B illustrates the nuclear mask 202 derived by the cell-based screening system. Figure 10C illustrates the cytoplasm 203 of the unstimulated cell imaged at a green wavelength. Figure 10D illustrates the nuclear mask 202 is eroded (reduced) once to define a nuclear sampling region 204 with minimal cytoplasmic distribution. The nucleus boundary 202 is dilated (expanded) several times to form a ring that is 2-3 pixels wide that is used to define the cytoplasmic sampling region 205 for the same cell. Figure 10E further illustrates a side view which shows the nuclear sampling region 204 and the cytoplasmic sampling region 205. Using these two sampling regions, data on nuclear translocation can be automatically analyzed by the cell-based screening system on a cell by cell basis. Figure 10F-J illustrates the strategy for determining nuclear translocation in a stimulated cell. Figure 10F illustrates a stimulated cell with its nucleus 206 labeled with a blue fluorophore and a transcription factor in the cytoplasm 207 labeled with a green fluorophore. The nuclear mask 208 in Figure 10G is derived by the cell based screening system. Figure 10H illustrates the cytoplasm 209 of a stimulated cell imaged at a green wavelength. Figure 10I illustrates the nuclear sampling region 211 and cytoplasmic sampling region 212 of the stimulated cell. Figure 10J further illustrates a side view which shows the nuclear sampling region 211 and the cytoplasmic sampling region 212.

A specific application of this method has been used to validate this method as a screen. A human cell line was plated in 96 well microtiter plates. Some rows of wells were titrated with IL-1, a known inducer of the NF-KB transcription factor. The cells were then fixed and stained by standard methods with a fluorescein labeled antibody to

the transcription factor, and Hoechst 33423. The cell-based screening system was used to acquire and analyze images from this plate and the NucCyt Difference was found to be strongly correlated with the amount of agonist added to the wells as illustrated in Figure 16. In a second experiment, an antagonist to the receptor for IL-1, IL-1RA was 5 titrated in the presence of IL-1 α , progressively inhibiting the translocation induced by IL-1 α . The NucCyt Difference was found to strongly correlate with this inhibition of translocation, as illustrated in Figure 17.

Additional experiments have shown that the NucCyt Difference, as well as the NucCyt ratio, gives consistent results over a wide range of cell densities and reagent 10 concentrations, and can therefore be routinely used to screen compound libraries for specific nuclear translocation activity. Furthermore, the same method can be used with antibodies to other transcription factors, or GFP-transcription factor chimeras, or fluorescently labeled transcription factors introduced into living or fixed cells, to screen for effects on the regulation of transcription factor activity.

15 **Figure 18** is a representative display on a PC screen of data which was obtained in accordance with Example 1. Graph 1 180 plots the difference between the average antibody fluorescence in the nuclear sampling region and cytoplasmic sampling region, NucCyt Difference versus Well #. Graph 2 181 plots the average fluorescence of the antibody in the nuclear sampling region, NP1 average, versus the Well #. Graph 3 182 20 plots the average antibody fluorescence in the cytoplasmic sampling region, LIP1 average, versus Well #. The software permits displaying data from each cell. For example, **Figure 18** shows a screen display 183, the nuclear image 184, and the fluorescent antibody image 185 for cell #26.

NucCyt Difference referred to in graph 1 180 of **Figure 18** is the difference 25 between the average cytoplasmic probe (fluorescent reporter molecule) intensity and the average nuclear probe (fluorescent reporter molecule) intensity. NP1 average referred to in graph 2 181 of **Figure 18** is the average of cytoplasmic probe (fluorescent reporter molecule) intensity within the nuclear sampling region. LIP1 average referred to in graph 3 182 of **Figure 18** is the average probe (fluorescent reporter molecule) 30 intensity within the cytoplasmic sampling region.

It will be understood by one of skill in the art that this aspect of the invention can be performed using other transcription factors that translocate from the cytoplasm

to the nucleus upon activation. In another specific example, activation of the c-fos transcription factor was assessed by defining its spatial position within cells. Activated c-fos is found only within the nucleus, while inactivated c-fos resides within the cytoplasm.

5 3T3 cells were plated at 5000-10000 cells per well in a Polyfiltronics 96-well plate. The cells were allowed to attach and grow overnight. The cells were rinsed twice with 100 µl serum-free medium, incubated for 24-30 hours in serum-free MEM culture medium, and then stimulated with platelet derived growth factor (PDGF-BB) (Sigma Chemical Co., St. Louis, MO) diluted directly into serum free medium at
10 concentrations ranging from 1-50 ng/ml for an average time of 20 minutes.

Following stimulation, cells were fixed for 20 minutes in 3.7% formaldehyde solution in 1X Hanks buffered saline solution (HBSS). After fixation, the cells were washed with HBSS to remove residual fixative, permeabilized for 90 seconds with 0.5% Triton X-100 solution in HBSS, and washed twice with HBSS to remove residual detergent. The cells were then blocked for 15 minutes with a 0.1% solution of BSA in HBSS, and further washed with HBSS prior to addition of diluted primary antibody solution.
15

c-Fos rabbit polyclonal antibody (Calbiochem, PC05) was diluted 1:50 in HBSS, and 50 µl of the dilution was applied to each well. Cells were incubated in the presence of primary antibody for one hour at room temperature, and then incubated for one hour at room temperature in a light tight container with goat anti-rabbit secondary antibody conjugated to ALEXA™ 488 (Molecular Probes), diluted 1:500 from a 100 µg/ml stock in HBSS. Hoechst DNA dye (Molecular Probes) was then added at a 1:1000 dilution of the manufacturer's stock solution (10 mg/ml). The cells were then
25 washed with HBSS, and the plate was sealed prior to analysis with the cell screening system of the invention. The data from these experiments demonstrated that the methods of the invention could be used to measure transcriptional activation of c-fos by defining its spatial position within cells.

One of skill in the art will recognize that while the following method is applied to
30 detection of c-fos activation, it can be applied to the analysis of any transcription factor that translocates from the cytoplasm to the nucleus upon activation. Examples of such transcription factors include, but are not limited to fos and jun homologs, NF-KB

(nuclear factor kappa from B cells), NFAT (nuclear factor of activated T-lymphocytes), and STATs (signal transducer and activator of transcription) factors (For example, see Strehlow, I., and Schindler, C. 1998. *J. Biol. Chem.* 273:28049-28056; Chow, et al. 1997 *Science*. 278:1638-1641; Ding et al. 1998 *J. Biol. Chem.* 273:28897-28905; 5 Baldwin, 1996. *Annu Rev Immunol.* 14:649-83; Kuo, C.T., and J.M. Leiden. 1999. *Annu Rev Immunol.* 17:149-87; Rao, et al. 1997. *Annu Rev Immunol.* 15:707-47; Masuda, et al. 1998. *Cell Signal.* 10:599-611; Hoey, T., and U. Schindler. 1998. *Curr Opin Genet Dev.* 8:582-7; Liu, et al. 1998. *Curr Opin Immunol.* 10:271-8.)

Thus, in this aspect of the invention, indicator cells are treated with test 10 compounds and the distribution of luminescently labeled transcription factor is measured in space and time using a cell screening system, such as the one disclosed above. The luminescently labeled transcription factor may be expressed by or added to the cells either before, together with, or after contacting the cells with a test compound.

For example, the transcription factor may be expressed as a luminescently 15 labeled protein chimera by transfected indicator cells. Alternatively, the luminescently labeled transcription factor may be expressed, isolated, and bulk-loaded into the indicator cells as described above, or the transcription factor may be luminescently labeled after isolation. As a further alternative, the transcription factor is expressed by the indicator cell, which is subsequently contacted with a luminescent label, such as an 20 antibody, that detects the transcription factor.

In a further aspect, kits are provided for analyzing transcription factor activation, comprising an antibody that specifically recognizes a transcription factor of interest, and instructions for using the antibody for carrying out the methods described above. In a preferred embodiment, the transcription factor-specific antibody, or a secondary 25 antibody that detects the transcription factor antibody, is luminescently labeled. In further preferred embodiments, the kit contains cells that express the transcription factor of interest, and/or the kit contains a compound that is known to modify activation of the transcription factor of interest, including but not limited to platelet derived growth factor (PDGF) and serum, which both modify fos activation; and interleukin 30 1(IL-1) and tumor necrosis factor (TNF), which both modify NF-KB activation.

In another embodiment, the kit comprises a recombinant expression vector comprising a nucleic acid encoding a transcription factor of interest that translocates

from the cytoplasm to the nucleus upon activation, and instructions for using the expression vector to identify compounds that modify transcription factor activation in a cell of interest. Alternatively, the kits contain a purified, luminescently labeled transcription factor. In a preferred embodiment, the transcription factor is expressed as
5 a fusion protein with a luminescent protein, including but not limited to green fluorescent protein, luciferase, or mutants or fragments thereof. In various preferred embodiments, the kit further contains cells that are transfected with the expression vector, an antibody or fragment that specifically bind to the transcription factor of interest, and/or a compound that is known to modify activation of the transcription
10 factor of interest (as above).

b. *Protein Kinases*

The cytoplasm to nucleus screening methods can also be used to analyze the activation of any protein kinase that is present in an inactive state in the cytoplasm and
15 is transported to the nucleus upon activation, or that phosphorylates a substrate that translocates from the cytoplasm to the nucleus upon phosphorylation. Examples of appropriate protein kinases include, but are not limited to extracellular signal-regulated protein kinases (ERKs), c-Jun amino-terminal kinases (JNKs), Fos regulating protein kinases (FRKs), p38 mitogen activated protein kinase (p38MAPK), protein kinase A
20 (PKA), and mitogen activated protein kinase kinases (MAPKKs). (For example, see Hall, et al. 1999. *J Biol Chem.* 274:376-83; Han, et al. 1995. *Biochim. Biophys. Acta.* 1265:224-227; Jaaro et al. 1997. *Proc. Natl. Acad. Sci. U.S.A.* 94:3742-3747; Taylor, et
al. 1994. *J. Biol. Chem.* 269:308-318; Zhao, Q., and F. S. Lee. 1999. *J Biol Chem.*
274:8355-8; Paolillo et al. 1999. *J Biol Chem.* 274:6546-52; Coso et al. 1995. *Cell*
25 81:1137-1146; Tibbles, L.A., and J.R. Woodgett. 1999. *Cell Mol Life Sci.* 55:1230-54;
Schaeffer, H.J., and M.J. Weber. 1999. *Mol Cell Biol.* 19:2435-44.)

Alternatively, protein kinase activity is assayed by monitoring translocation of a luminescently labeled protein kinase substrate from the cytoplasm to the nucleus after being phosphorylated by the protein kinase of interest. In this embodiment, the
30 substrate is non-phosphorylated and cytoplasmic prior to phosphorylation, and is translocated to the nucleus upon phosphorylation by the protein kinase. There is no requirement that the protein kinase itself translocates from the cytoplasm to the nucleus

in this embodiment. Examples of such substrates (and the corresponding protein kinase) include, but are not limited to c-jun (JNK substrate); fos (FRK substrate), and p38 (p38 MAPK substrate).

Thus, in these embodiments, indicator cells are treated with test compounds and
5 the distribution of luminescently labeled protein kinase or protein kinase substrate is measured in space and time using a cell screening system, such as the one disclosed above. The luminescently labeled protein kinase or protein kinase substrate may be expressed by or added to the cells either before, together with, or after contacting the cells with a test compound. For example, the protein kinase or protein kinase substrate
10 may be expressed as a luminescently labeled protein chimera by transfected indicator cells. Alternatively, the luminescently labeled protein kinase or protein kinase substrate may be expressed, isolated, and bulk-loaded into the indicator cells as described above, or the protein kinase or protein kinase substrate may be luminescently labeled after isolation. As a further alternative, the protein kinase or protein kinase
15 substrate is expressed by the indicator cell, which is subsequently contacted with a luminescent label, such as a labeled antibody, that detects the protein kinase or protein kinase substrate.

In a further embodiment, protein kinase activity is assayed by monitoring the phosphorylation state (ie: phosphorylated or not phosphorylated) of a protein kinase substrate. In this embodiment, there is no requirement that either the protein kinase or the protein kinase substrate translocate from the cytoplasm to the nucleus upon activation. In a preferred embodiment, phosphorylation state is monitored by contacting the cells with an antibody that binds only to the phosphorylated form of the protein kinase substrate of interest (For example, as disclosed in U.S. Patent No.
25 5,599,681).

In another preferred embodiment, a biosensor of phosphorylation is used. For example, a luminescently labeled protein or fragment thereof can be fused to a protein that has been engineered to contain (a) a phosphorylation site that is recognized by a protein kinase of interest; and (b) a nuclear localization signal that is unmasked by the
30 phosphorylation. Such a biosensor will thus be translocated to the nucleus upon phosphorylation, and its translocation can be used as a measure of protein kinase activation.

In another aspect, kits are provided for analyzing protein kinase activation, comprising a primary antibody that specifically binds to a protein kinase, a protein kinase substrate, or a phosphorylated form of the protein kinase substrate of interest and instructions for using the primary antibody to identify compounds that modify protein

5 kinase activation in a cell of interest. In a preferred embodiment, the primary antibody, or a secondary antibody that detects the primary antibody, is luminescently labeled. In other preferred embodiments, the kit further comprises cells that express the protein kinase of interest, and/or a compound that is known to modify activation of the protein kinase of interest, including but not limited to dibutyryl cAMP (modifies PKA),

10 forskolin (PKA), and anisomycin (p38MAPK).

Alternatively, the kits comprise an expression vector encoding a protein kinase or a protein kinase substrate of interest that translocates from the cytoplasm to the nucleus upon activation and instructions for using the expression vector to identify compounds that modify protein kinase activation in a cell of interest. Alternatively, the

15 kits contain a purified, luminescently labeled protein kinase or protein kinase substrate. In a preferred embodiment, the protein kinase or protein kinase substrate of interest is expressed as a fusion protein with a luminescent protein. In further preferred embodiments, the kit further comprises cells that are transfected with the expression vector, an antibody or fragment thereof that specifically binds to the protein kinase or

20 protein kinase substrate of interest, and/or a compound that is known to modify activation of the protein kinase of interest. (as above)

In another aspect, the present invention comprises a machine readable storage medium comprising a program containing a set of instructions for causing a cell screening system to execute the methods disclosed for analyzing transcription factor or

25 protein kinase activation, wherein the cell screening system comprises an optical system with a stage adapted for holding a plate containing cells, a digital camera, a means for directing fluorescence or luminescence emitted from the cells to the digital camera, and a computer means for receiving and processing the digital data from the digital camera.

Example 2 Automated Screen for Compounds that Modify Cellular Morphology

Changes in cell size are associated with a number of cellular conditions, such as hypertrophy, cell attachment and spreading, differentiation, growth and division, necrotic and programmed cell death, cell motility, morphogenesis, tube formation, and 5 colony formation.

For example, cellular hypertrophy has been associated with a cascade of alterations in gene expression and can be characterized in cell culture by an alteration in cell size, that is clearly visible in adherent cells growing on a coverslip.

Cell size can also be measured to determine the attachment and spreading of 10 adherent cells. Cell spreading is the result of selective binding of cell surface receptors to substrate ligands and subsequent activation of signaling pathways to the cytoskeleton. Cell attachment and spreading to substrate molecules is an important step for the metastasis of cancer cells, leukocyte activation during the inflammatory response, keratinocyte movement during wound healing, and endothelial cell 15 movement during angiogenesis. Compounds that affect these surface receptors, signaling pathways, or the cytoskeleton will affect cell spreading and can be screened by measuring cell size.

Total cellular area can be monitored by labeling the entire cell body or the cell 20 cytoplasm using cytoskeletal markers, cytosolic volume markers, or cell surface markers, in conjunction with a DNA label. Examples of such labels (many available from Molecular Probes (Eugene, Oregon) and Sigma Chemical Co. (St. Louis, Missouri)) include the following:

CELL SIZE AND AREA MARKERS	
Cytoskeletal Markers	
<ul style="list-style-type: none"> • ALEXA™ 488 phalloidin (Molecular Probes, Oregon) • Tubulin-green fluorescent protein chimeras • Cytokeratin-green fluorescent protein chimeras • Antibodies to cytoskeletal proteins 	
Cytosolic Volume Markers	
<ul style="list-style-type: none"> • Green fluorescent proteins • Chloromethylfluorescein diacetate (CMFDA) • Calcein green • BCECF/AM ester • Rhodamine dextran 	
Cell Surface Markers for Lipid, Protein, or Oligosaccharide	
<ul style="list-style-type: none"> • Dihexadecyl tetramethylindocarbocyanine perchlorate (DiIC16) lipid dyes • Triethylammonium propyl dibutylamino styryl pyridinium (FM 4-64, FM 1-43) lipid dyes • MITOTRACKER™ Green FM • Lectins to oligosaccharides such as fluorescein concanavalin A or wheat germ agglutinin • SYPRO™ Red non-specific protein markers • Antibodies to various surface proteins such as epidermal growth factor • Biotin labeling of surface proteins followed by fluorescent streptavidin labeling 	

Protocols for cell staining with these various agents are well known to those skilled in the art. Cells are stained live or after fixation and the cell area can be measured. For example, live cells stained with DiIC16 have homogeneously labeled plasma membranes, and the projected cross-sectional area of the cell is uniformly discriminated from background by fluorescence intensity of the dye. Live cells stained with cytosolic stains such as CMFDA produce a fluorescence intensity that is proportional to cell thickness. Although cell labeling is dimmer in thin regions of the cell, total cell area can be discriminated from background. Fixed cells can be stained with cytoskeletal markers such as ALEXA™ 488 phalloidin that label polymerized actin. Phalloidin does not homogeneously stain the cytoplasm, but still permits discrimination of the total cell area from background.

15 *Cellular hypertrophy*

A screen to analyze cellular hypertrophy is implemented using the following strategy. Primary rat myocytes can be cultured in 96 well plates, treated with various compounds and then fixed and labeled with a fluorescent marker for the cell membrane or cytoplasm, or cytoskeleton, such as an antibody to a cell surface marker or a

fluorescent marker for the cytoskeleton like rhodamine-phalloidin, in combination with a DNA label like Hoechst.

After focusing on the Hoechst labeled nuclei, two images are acquired, one of the Hoechst labeled nuclei and one of the fluorescent cytoplasm image. The nuclei are
5 identified by thresholding to create a mask and then comparing the morphological descriptors of the mask with a set of user defined descriptor values. Each non-nucleus image (or "cytoplasmic image") is then processed separately. The original cytoplasm image can be thresholded, creating a cytoplasmic mask image. Local regions containing cells are defined around the nuclei. The limits of the cells in those regions are then
10 defined by a local dynamic threshold operation on the same region in the fluorescent antibody image. A sequence of erosions and dilations is used to separate slightly touching cells and a second set of morphological descriptors is used to identify single cells. The area of the individual cells is tabulated in order to define the distribution of cell sizes for comparison with size data from normal and hypertrophic cells.

15 Responses from entire 96-well plates (measured as average cytoplasmic area/cell) were analyzed by the above methods, and the results demonstrated that the assay will perform the same on a well-to-well, plate-to-plate, and day-to-day basis (below a 15% cov for maximum signal). The data showed very good correlation for each day, and that there was no variability due to well position in the plate.

20 The following totals can be computed for the field. The aggregate whole nucleus area is the number of nonzero pixels in the nuclear mask. The average whole nucleus area is the aggregate whole nucleus area divided by the total number of nuclei. For each cytoplasm image several values can be computed. These are the total cytoplasmic area, which is the count of nonzero pixels in the cytoplasmic mask. The
25 aggregate cytoplasm intensity is the sum of the intensities of all pixels in the cytoplasmic mask. The cytoplasmic area per nucleus is the total cytoplasmic area divided by the total nucleus count. The cytoplasmic intensity per nucleus is the aggregate cytoplasm intensity divided by the total nucleus count. The average cytoplasm intensity is the aggregate cytoplasm intensity divided by the cytoplasm area.
30 The cytoplasm nucleus ratio is the total cytoplasm area divided by the total nucleus area.

Additionally, one or more fluorescent antibodies to other cellular proteins, such as the major muscle proteins actin or myosin, can be included. Images of these additional labeled proteins can be acquired and stored with the above images, for later review, to identify anomalies in the distribution and morphology of these proteins in hypertrophic cells. This example of a multi-parametric screen allows for simultaneous analysis of cellular hypertrophy and changes in actin or myosin distribution.

One of skill in the art will recognize that while the example analyzes myocyte hypertrophy, the methods can be applied to analyzing hypertrophy, or general morphological changes in any cell type.

10

Cell morphology assays for prostate carcinoma

Cell spreading is a measure of the response of cell surface receptors to substrate attachment ligands. Spreading is proportional to the ligand concentration or to the concentration of compounds that reduce receptor-ligand function. One example of selective cell-substrate attachment is prostate carcinoma cell adhesion to the extracellular matrix protein collagen. Prostate carcinoma cells metastasize to bone via selective adhesion to collagen.

Compounds that interfere with metastasis of prostate carcinoma cells were screened as follows. PC3 human prostate carcinoma cells were cultured in media with appropriate stimulants and are passaged to collagen coated 96 well plates. Ligand concentration can be varied or inhibitors of cell spreading can be added to the wells. Examples of compounds that can affect spreading are receptor antagonists such as integrin- or proteoglycan-blocking antibodies, signaling inhibitors including phosphatidyl inositol-3 kinase inhibitors, and cytoskeletal inhibitors such as cytochalasin D. After two hours, cells were fixed and stained with ALEXA™ 488 phalloidin (Molecular Probes) and Hoechst 33342 as per the protocol for cellular hypertrophy. The size of cells under these various conditions, as measured by cytoplasmic staining, can be distinguished above background levels. The number of cells per field is determined by measuring the number of nuclei stained with the Hoechst DNA dye. The area per cell is found by dividing the cytoplasmic area (phalloidin image) by the cell number (Hoechst image). The size of cells is proportional to the ligand-receptor function. Since the area is determined by ligand

concentration and by the resultant function of the cell, drug efficacy, as well as drug potency, can be determined by this cell-based assay. Other measurements can be made as discussed above for cellular hypertrophy.

The methods for analyzing cellular morphology can be used in a combined high throughput-high content screen. In one example, the high throughput mode scans the whole well for an increase in fluorescent phalloidin intensity. A threshold is set above which both nuclei (Hoechst) and cells (phalloidin) are measured in a high content mode. In another example, an environmental biosensor (examples include, but are not limited to, those biosensors that are sensitive to calcium and pH changes) is added to the cells, and the cells are contacted with a compound. The cells are scanned in a high throughput mode, and those wells that exceed a pre-determined threshold for luminescence of the biosensor are scanned in a high content mode.

In a further aspect, kits are provided for analyzing cellular morphology, comprising a luminescent compound that can be used to specifically label the cell cytoplasm, membrane, or cytoskeleton (such as those described above), and instructions for using the luminescent compound to identify test stimuli that induce or inhibit changes in cellular morphology according to the above methods. In a preferred embodiment, the kit further comprises a luminescent marker for cell nuclei. In a further preferred embodiment, the kit comprises at least one compound that is known to modify cellular morphology, including, but not limited to integrin- or proteoglycan-blocking antibodies, signaling inhibitors including phosphatidyl inositol-3 kinase inhibitors, and cytoskeletal inhibitors such as cytochalasin D.

In another aspect, the present invention comprises a machine readable storage medium comprising a program containing a set of instructions for causing a cell screening system to execute the disclosed methods for analyzing cellular morphology, wherein the cell screening system comprises an optical system with a stage adapted for holding a plate containing cells, a digital camera, a means for directing fluorescence or luminescence emitted from the cells to the digital camera, and a computer means for receiving and processing the digital data from the digital camera.

30 *Example 3 Dual Mode High Throughput and High-Content Screen*

The following example is a screen for activation of a G-protein coupled receptor (GPCR) as detected by the translocation of the GPCR from the plasma membrane to a

proximal nuclear location. This example illustrates how a high throughput screen can be coupled with a high-content screen in the dual mode System for Cell Based Screening.

G-protein coupled receptors are a large class of 7 trans-membrane domain cell surface receptors. Ligands for these receptors stimulate a cascade of secondary signals in the cell, which may include, but are not limited to, Ca^{++} transients, cyclic AMP production, inositol triphosphate (IP_3) production and phosphorylation. Each of these signals are rapid, occurring in a matter of seconds to minutes, but are also generic. For example, many different GPCRs produce a secondary Ca^{++} signal when activated. Stimulation of a GPCR also results in the transport of that GPCR from the cell surface membrane to an internal, proximal nuclear compartment. This internalization is a much more receptor-specific indicator of activation of a particular receptor than are the secondary signals described above.

Figure 19 illustrates a dual mode screen for activation of a GPCR. Cells carrying a stable chimera of the GPCR with a blue fluorescent protein (BFP) would be loaded with the acetoxymethylene form of Fluo-3, a cell permeable calcium indicator (green fluorescence) that is trapped in living cells by the hydrolysis of the esters. They would then be deposited into the wells of a microtiter plate 601. The wells would then be treated with an array of test compounds using a fluid delivery system, and a short sequence of Fluo-3 images of the whole microtiter plate would be acquired and analyzed for wells exhibiting a calcium response (i.e., high throughput mode). The images would appear like the illustration of the microtiter plate 601 in Figure 19. A small number of wells, such as wells C4 and E9 in the illustration, would fluoresce more brightly due to the Ca^{++} released upon stimulation of the receptors. The locations of wells containing compounds that induced a response 602, would then be transferred to the HCS program and the optics switched for detailed cell by cell analysis of the blue fluorescence for evidence of GPCR translocation to the perinuclear region. The bottom of Figure 19 illustrates the two possible outcomes of the analysis of the high resolution cell data. The camera images a sub-region 604 of the well area 603, producing images of the fluorescent cells 605. In well C4, the uniform distribution of the fluorescence in the cells indicates that the receptor has not internalized, implying that the Ca^{++} response

seen was the result of the stimulation of some other signalling system in the cell. The cells in well E9 606 on the other hand, clearly indicate a concentration of the receptor in the perinuclear region clearly indicating the full activation of the receptor. Because only a few hit wells have to be analyzed with high resolution, the overall throughput of 5 the dual mode system can be quite high, comparable to the high throughput system alone.

Example 4 Kinetic High Content Screen

The following is an example of a screen to measure the kinetics of 10 internalization of a receptor. As described above, the stimulation of a GPCR, results in the internalization of the receptor, with a time course of about 15 min. Simply detecting the endpoint as internalized or not, may not be sufficient for defining the potency of a compound as a GPCR agonist or antagonist. However, 3 time points at 5 min intervals would provide information not only about potency during the time course 15 of measurement, but would also allow extrapolation of the data to much longer time periods. To perform this assay, the sub-region would be defined as two rows, the sampling interval as 5 minutes and the total number of time points 3. The system would then start by scanning two rows, and then adding reagent to the two rows, establishing the time=0 reference. After reagent addition, the system would again scan 20 the two row sub-region acquiring the first time point data. Since this process would take about 250 seconds, including scanning back to the beginning of the sub-region, the system would wait 50 seconds to begin acquisition of the second time point. Two more cycles would produce the three time points and the system would move on to the second 2 row sub-region. The final two 2-row sub-regions would be scanned to finish 25 all the wells on the plate, resulting in four time points for each well over the whole plate. Although the time points for the wells would be offset slightly relative to time=0, the spacing of the time points would be very close to the required 5 minutes, and the actual acquisition times and results recorded with much greater precision than in a fixed-cell screen.

Example 5 High-content screen of human glucocorticoid receptor translocation

One class of HCS involves the drug-induced dynamic redistribution of intracellular constituents. The human glucocorticoid receptor (hGR), a single "sensor" in the complex environmental response machinery of the cell, binds steroid molecules
5 that have diffused into the cell. The ligand-receptor complex translocates to the nucleus where transcriptional activation occurs (Htun et al., *Proc. Natl. Acad. Sci.* 93:4845, 1996).

In general, hormone receptors are excellent drug targets because their activity lies at the apex of key intracellular signaling pathways. Therefore, a high-content
10 screen of hGR translocation has distinct advantage over *in vitro* ligand-receptor binding assays. The availability of up to two more channels of fluorescence in the cell screening system of the present invention permits the screen to contain two additional parameters in parallel, such as other receptors, other distinct targets or other cellular processes.

15 **Plasmid construct.** A eukaryotic expression plasmid containing a coding sequence for a green fluorescent protein – human glucocorticoid receptor (GFP-hGR) chimera was prepared using GFP mutants (Palm et al., *Nat. Struct. Biol.* 4:361 (1997). The construct was used to transfet a human cervical carcinoma cell line (HeLa).

Cell preparation and transfection. HeLa cells (ATCC CCL-2) were trypsinized
20 and plated using DMEM containing 5% charcoal/dextran-treated fetal bovine serum (FBS) (HyClone) and 1% penicillin-streptomycin (C-DMEM) 12-24 hours prior to transfection and incubated at 37°C and 5% CO₂. Transfections were performed by calcium phosphate co-precipitation (Graham and Van der Eb, *Virology* 52:456, 1973; Sambrook et al., (1989). *Molecular Cloning: A Laboratory Manual*, Second ed. Cold
25 Spring Harbor Laboratory Press, Cold Spring Harbor, 1989) or with Lipofectamine (Life Technologies, Gaithersburg, MD). For the calcium phosphate transfections, the medium was replaced, prior to transfection, with DMEM containing 5% charcoal/dextran-treated FBS. Cells were incubated with the calcium phosphate-DNA precipitate for 4-5 hours at 37°C and 5% CO₂, washed 3-4 times with DMEM to
30 remove the precipitate, followed by the addition of C-DMEM.

Lipofectamine transfections were performed in serum-free DMEM without antibiotics according to the manufacturer's instructions (Life Technologies,

Gaithersburg, MD). Following a 2-3 hour incubation with the DNA-liposome complexes, the medium was removed and replaced with C-DMEM. All transfected cells in 96-well microtiter plates were incubated at 33°C and 5% CO₂ for 24-48 hours prior to drug treatment. Experiments were performed with the receptor expressed transiently in HeLa cells.

5 *Dexamethasone induction of GFP-hGR translocation.* To obtain receptor-ligand translocation kinetic data, nuclei of transfected cells were first labeled with 5 µg/ml Hoechst 33342 (Molecular Probes) in C-DMEM for 20 minutes at 33°C and 5% CO₂. Cells were washed once in Hank's Balanced Salt Solution (HBSS) followed by
10 the addition of 100 nM dexamethasone in HBSS with 1% charcoal/dextran-treated FBS. To obtain fixed time point dexamethasone titration data, transfected HeLa cells were first washed with DMEM and then incubated at 33°C and 5% CO₂ for 1 h in the presence of 0 – 1000 nM dexamethasone in DMEM containing 1% charcoal/dextran-treated FBS. Cells were analyzed live or they were rinsed with HBSS, fixed for 15 min
15 with 3.7% formaldehyde in HBSS, stained with Hoechst 33342, and washed before analysis. The intracellular GFP-hGR fluorescence signal was not diminished by this fixation procedure.

20 *Image acquisition and analysis.* Kinetic data were collected by acquiring fluorescence image pairs (GFP-hGR and Hoechst 33342-labeled nuclei) from fields of living cells at 1 min intervals for 30 min after the addition of dexamethasone. Likewise, image pairs were obtained from each well of the fixed time point screening plates 1 h after the addition of dexamethasone. In both cases, the image pairs obtained at each time point were used to define nuclear and cytoplasmic regions in each cell. Translocation of GFP-hGR was calculated by dividing the integrated fluorescence
25 intensity of GFP-hGR in the nucleus by the integrated fluorescence intensity of the chimera in the cytoplasm or as a nuclear-cytoplasmic difference of GFP fluorescence. In the fixed time point screen this translocation ratio was calculated from data obtained from at least 200 cells at each concentration of dexamethasone tested. Drug-induced translocation of GFP-hGR from the cytoplasm to the nucleus was therefore correlated
30 with an increase in the translocation ratio.

Results. Figure 20 schematically displays the drug-induced cytoplasm 253 to nucleus 252 translocation of the human glucocorticoid receptor. The upper pair of

- schematic diagrams depicts the localization of GFP-hGR within the cell before 250 (A) and after 251 (B) stimulation with dexamethasone. Under these experimental conditions, the drug induces a large portion of the cytoplasmic GFP-hGR to translocate into the nucleus. This redistribution is quantified by determining the integrated intensities ratio of the cytoplasmic and nuclear fluorescence in treated 255 and untreated 254 cells. The lower pair of fluorescence micrographs show the dynamic redistribution of GFP-hGR in a single cell, before 254 and after 255 treatment. The HCS is performed on wells containing hundreds to thousands of transfected cells and the translocation is quantified for each cell in the field exhibiting GFP fluorescence.
- 5 Although the use of a stably transfected cell line would yield the most consistently labeled cells, the heterogeneous levels of GFP-hGR expression induced by transient transfection did not interfere with analysis by the cell screening system of the present invention.
- 10

To execute the screen, the cell screening system scans each well of the plate, images a population of cells in each, and analyzes cells individually. Here, two channels of fluorescence are used to define the cytoplasmic and nuclear distribution of the GFP-hGR within each cell. Depicted in Figure 21 is the graphical user interface of the cell screening system near the end of a GFP-hGR screen. The user interface depicts the parallel data collection and analysis capability of the system. The windows labeled "Nucleus" 261 and "GFP-hGR" 262 show the pair of fluorescence images being obtained and analyzed in a single field. The window labeled "Color Overlay" 260 is formed by pseudocoloring the above images and merging them so the user can immediately identify cellular changes. Within the "Stored Object Regions" window 265, an image containing each analyzed cell and its neighbors is presented as it is archived. Furthermore, as the HCS data are being collected, they are analyzed, in this case for GFP-hGR translocation, and translated into an immediate "hit" response. The 96 well plate depicted in the lower window of the screen 267 shows which wells have met a set of user-defined screening criteria. For example, a white-colored well 269 indicates that the drug-induced translocation has exceeded a predetermined threshold value of 50%. On the other hand, a black-colored well 270 indicates that the drug being tested induced less than 10% translocation. Gray-colored wells 268 indicate "hits" where the translocation value fell between 10% and 50%. Row "E" on the 96 well

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plate being analyzed 266 shows a titration with a drug known to activate GFP-hGR translocation, dexamethasone. This example screen used only two fluorescence channels. Two additional channels (Channels 3 263 and 4 264) are available for parallel analysis of other specific targets, cell processes, or cytotoxicity to create 5 multiple parameter screens.

There is a link between the image database and the information database that is a powerful tool during the validation process of new screens. At the completion of a screen, the user has total access to image and calculated data (Figure 22). The comprehensive data analysis package of the cell screening system allows the user to 10 examine HCS data at multiple levels. Images 276 and detailed data in a spread sheet 279 for individual cells can be viewed separately, or summary data can be plotted. For example, the calculated results of a single parameter for each cell in a 96 well plate are shown in the panel labeled Graph 1 275. By selecting a single point in the graph, the user can display the entire data set for a particular cell that is recalled from an existing 15 database. Shown here are the image pair 276 and detailed fluorescence and morphometric data from a single cell (Cell #118, gray line 277). The large graphical insert 278 shows the results of dexamethasone concentration on the translocation of GFP-hGR. Each point is the average of data from at least 200 cells. The calculated EC₅₀ for dexamethasone in this assay is 2 nM.

20 A powerful aspect of HCS with the cell screening system is the capability of kinetic measurements using multicolor fluorescence and morphometric parameters in living cells. Temporal and spatial measurements can be made on single cells within a population of cells in a field. Figure 23 shows kinetic data for the dexamethasone-induced translocation of GFP-hGR in several cells within a single field. Human HeLa 25 cells transfected with GFP-hGR were treated with 100 nM dexamethasone and the translocation of GFP-hGR was measured over time in a population of single cells. The graph shows the response of transfected cells 285, 286, 287, and 288 and non-transfected cells 289. These data also illustrate the ability to analyze cells with different expression levels.

Example 6 High-content screen of drug-induced apoptosis

Apoptosis is a complex cellular program that involves myriad molecular events and pathways. To understand the mechanisms of drug action on this process, it is essential to measure as many of these events within cells as possible with temporal and spatial resolution. Therefore, an apoptosis screen that requires little cell sample preparation yet provides an automated readout of several apoptosis-related parameters would be ideal. A cell-based assay designed for the cell screening system has been used to simultaneously quantify several of the morphological, organellar, and macromolecular hallmarks of paclitaxel-induced apoptosis.

Cell preparation. The cells chosen for this study were mouse connective tissue fibroblasts (L-929; ATCC CCL-1) and a highly invasive glioblastoma cell line (SNB-19; ATCC CRL-2219) (Welch et al., *In Vitro Cell. Dev. Biol.* 31:610, 1995). The day before treatment with an apoptosis inducing drug, 3500 cells were placed into each well of a 96-well plate and incubated overnight at 37°C in a humidified 5% CO₂ atmosphere. The following day, the culture medium was removed from each well and replaced with fresh medium containing various concentrations of paclitaxel (0 – 50 µM) from a 20 mM stock made in DMSO. The maximal concentration of DMSO used in these experiments was 0.25%. The cells were then incubated for 26 h as above. At the end of the paclitaxel treatment period, each well received fresh medium containing 750 nM MitoTracker Red (Molecular Probes; Eugene, OR) and 3 µg/ml Hoechst 33342 DNA-binding dye (Molecular Probes) and was incubated as above for 20 min. Each well on the plate was then washed with HBSS and fixed with 3.7% formaldehyde in HBSS for 15 min at room temperature. The formaldehyde was washed out with HBSS and the cells were permeabilized for 90 s with 0.5% (v/v) Triton X-100, washed with HBSS, incubated with 2 U ml⁻¹ Bodipy FL phallacidin (Molecular Probes) for 30 min, and washed with HBSS. The wells on the plate were then filled with 200 µl HBSS, sealed, and the plate stored at 4°C if necessary. The fluorescence signals from plates stored this way were stable for at least two weeks after preparation. As in the nuclear translocation assay, fluorescence reagents can be designed to convert this assay into a live cell high-content screen.

Image acquisition and analysis on the ArrayScan System. The fluorescence intensity of intracellular MitoTracker Red, Hoechst 33342, and Bodipy FL phallacidin

was measured with the cell screening system as described *supra*. Morphometric data from each pair of images obtained from each well was also obtained to detect each object in the image field (e.g., cells and nuclei), and to calculate its size, shape, and integrated intensity.

5 *Calculations and output.* A total of 50-250 cells were measured per image field. For each field of cells, the following calculations were performed: (1) The average nuclear area (μm^2) was calculated by dividing the total nuclear area in a field by the number of nuclei detected. (2) The average nuclear perimeter (μm) was calculated by dividing the sum of the perimeters of all nuclei in a field by the number
10 of nuclei detected in that field. Highly convoluted apoptotic nuclei had the largest nuclear perimeter values. (3) The average nuclear brightness was calculated by dividing the integrated intensity of the entire field of nuclei by the number of nuclei in that field. An increase in nuclear brightness was correlated with increased DNA content. (4) The average cellular brightness was calculated by dividing the integrated intensity of an
15 entire field of cells stained with MitoTracker dye by the number of nuclei in that field. Because the amount of MitoTracker dye that accumulates within the mitochondria is proportional to the mitochondrial potential, an increase in the average cell brightness is consistent with an increase in mitochondrial potential. (5) The average cellular brightness was also calculated by dividing the integrated intensity of an entire field of
20 cells stained with Bodipy FL phallacidin dye by the number of nuclei in that field. Because the phalloidins bind with high affinity to the polymerized form of actin, the amount of Bodipy FL phallacidin dye that accumulates within the cell is proportional to actin polymerization state. An increase in the average cell brightness is consistent with an increase in actin polymerization.

25 *Results.* Figure 24 (top panels) shows the changes paclitaxel induced in the nuclear morphology of L-929 cells. Increasing amounts of paclitaxel caused nuclei to enlarge and fragment 293, a hallmark of apoptosis. Quantitative analysis of these and other images obtained by the cell screening system is presented in the same figure. Each parameter measured showed that the L-929 cells 296 were less sensitive to low
30 concentrations of paclitaxel than were SNB-19 cells 297. At higher concentrations though, the L-929 cells showed a response for each parameter measured. The multiparameter approach of this assay is useful in dissecting the mechanisms of drug

action. For example, the area, brightness, and fragmentation of the nucleus 298 and actin polymerization values 294 reached a maximum value when SNB-19 cells were treated with 10 nM paclitaxel (Figure 24; top and bottom graphs). However, mitochondrial potential 295 was minimal at the same concentration of paclitaxel
5 (Figure 24; middle graph). The fact that all the parameters measured approached control levels at increasing paclitaxel concentrations (>10 nM) suggests that SNB-19 cells have low affinity drug metabolic or clearance pathways that are compensatory at sufficiently high levels of the drug. Contrasting the drug sensitivity of SNB-19 cells
297, L-929 showed a different response to paclitaxel 296. These fibroblastic cells
10 showed a maximal response in many parameters at 5 μ M paclitaxel, a 500-fold higher dose than SNB-19 cells. Furthermore, the L-929 cells did not show a sharp decrease in mitochondrial potential 295 at any of the paclitaxel concentrations tested. This result is consistent with the presence of unique apoptosis pathways between a normal and cancer cell line. Therefore, these results indicate that a relatively simple fluorescence
15 labeling protocol can be coupled with the cell screening system of the present invention to produce a high-content screen of key events involved in programmed cell death.

Background

A key to the mechanism of apoptosis was the discovery that, irrespective of the
20 lethal stimulus, death results in identical apoptotic morphology that includes cell and organelle dismantling and repackaging, DNA cleavage to nucleosome sized fragments, and engulfment of the fragmented cell to avoid an inflammatory response. Apoptosis is therefore distinct from necrosis, which is mediated more by acute trauma to a cell, resulting in spillage of potentially toxic and antigenic cellular components into the
25 intercellular milieu, leading to an inflammatory response.

The criteria for determining whether a cell is undergoing apoptosis (Wyllie et al. 1980. *Int Rev Cytol.* 68:251-306; Thompson, 1995. *Science.* 267:1456-62; Majno and Joris. 1995. *Am J Pathol.* 146:3-15; Allen et al. 1998. *Cell Mol Life Sci.* 54:427-45) include distinct morphological changes in the appearance of the cell, as well as
30 alterations in biochemical and molecular markers. For example, apoptotic cells often undergo cytoplasmic membrane blebbing, their chromosomes rapidly condense and

aggregate around the nuclear periphery, the nucleus fragments, and small apoptotic bodies are formed. In many, but not all, apoptotic cells, chromatin becomes a target for specific nucleases that cleave the DNA.

Apoptosis is commonly accompanied by a characteristic change in nuclear morphology (chromatin condensation or fragmentation) and a step-wise fragmentation of DNA culminating in the formation of mono- and/or oligomeric fragments of 200 base pairs. Specific changes in organellar function, such as mitochondrial membrane potential, occur. In addition, specific cysteine proteases (caspases) are activated, which catalyzes a highly selective pattern of protein degradation by proteolytic cleavage after specific aspartic acid residues. In addition, the external surface exposure of phosphatidylserine residues (normally on the inner membrane leaflet) allows for the recognition and elimination of apoptotic cells, before the membrane breaks up and cytosol or organelles spill into the intercellular space and elicit inflammatory reactions. Moreover, cells undergoing apoptosis tend to shrink, while also having a reduced intracellular potassium level.

The general patterns of apoptotic signals are very similar among different cell types and apoptotic inducers. However, the details of the pathways actually vary significantly depending on cell type and inducer. The dependence and independence of various signal transduction pathways involved in apoptosis are currently topics of intense research. We show here that the pathway also varies depending upon the dose of the inducer in specific cell types.

Nuclear Morphology

Cells undergoing apoptosis generally exhibit two types of nuclear change, fragmentation or condensation ((Majno and Joris, 1995), (Earnshaw, 1995)). The response in a given cell type appears to vary depending on the apoptotic inducer. During nuclear fragmentation, a circular or oval nucleus becomes increasingly lobular. Eventually, the nucleus fragments dramatically into multiple sub-nuclei. Sometimes the density of the chromatin within the lobular nucleus may show spatial variations in distribution (heterochromatization), approximating the margination seen in nuclear condensation.

Nuclear condensation has been reported in some cell types, such as MCF-7 (Saunders et al. 1997. *Int J Cancer.* 70:214-20). Condensation appears to arise as a consequence of the loss of structural integrity of the euchromatin, nuclear matrix and nuclear lamina (Hendzel et al. 1998. *J Biol Chem.* 273:24470-8). During nuclear
5 condensation, the chromatin concentrates near the margin of the nucleus, leading to the overall shrinkage of the nucleus. Thus, the use of nuclear morphology as a measure of apoptosis must take both condensation and fragmentation into account.

Material and Methods

10 Cells were plated into 96-well plates at densities of 3×10^3 to 1×10^4 cells/well. The following day apoptotic inducers were added at indicated concentrations and cells were incubated for indicated time periods (usually 16-30 hours). The next day medium was removed and cells were stained with 5 µg/ml Hoechst (Molecular Probes, Inc.) in fresh medium and incubated for 30 minutes at 37°C. Cells were washed in Hank's
15 Balanced Salt Solution (HBSS) and fixed with 3.7% formaldehyde in HBSS at room temperature. Cells were washed 2X with HBSS at room temperature and the plate was sealed.

Quantitation of changes in nuclear morphology upon induction of apoptosis was accomplished by (1) measuring the effective size of the nuclear region; and (2)
20 measuring the degree of convolution of the perimeter. The size parameter provides the more sensitive measure of nuclear condensation, whereas the perimeter measure provides a more sensitive measure of nuclear fragmentation.

Results & Discussion

25 L929 cells responded to both staurosporine (30 hours) and paclitaxel (30 hours) with a dose-dependent change in nuclear morphology (Fig 25A and 25B). BHK cells illustrated a slightly more complicated, yet clearly visible response. Staurosporine appeared to stimulate nuclear condensation at lower doses and nuclear fragmentation at higher doses (Fig 25C and 25D). In contrast, paclitaxel induced a consistent increase in
30 nuclear fragmentation with increasing concentrations. The response of MCF-7 cells varied dramatically depending upon the apoptotic inducer. Staurosporine appeared to

elicit nuclear condensation whereas paclitaxel induced nuclear fragmentation (Fig 25E and 25F).

Figure 26 illustrates the dose response of cells in terms of both nuclear size and nuclear perimeter convolution. There appears to be a swelling of the nuclei that precedes the fragmentation.

Result of evaluation: Differential responses by cell lines and by apoptotic inducers were observed in a dose dependent manner, indicating that this assay will be useful for detecting changes in the nucleus characteristic of apoptosis.

10 Actin reorganization

We assessed changes in the actin cytoskeleton as a potential parameter related to apoptotic changes. This was based on preliminary observations of an early increase in f-actin content detected with fluorescent phalloidin labeling, an f-actin specific stain (our unpublished data; Levee et al. 1996. *Am J Physiol.* 271:C1981-92; Maekawa et al. 1996. *Clin Exp Immunol.* 105:389-96). Changes in the actin cytoskeleton during apoptosis have not been observed in all cell types. (Endresen et al. 1995. *Cytometry*. 20:162-71, van Engeland et al. 1997. *Exp Cell Res.* 235:421-30).

Material and Methods

Cells were plated in 96-well plates at densities of 3×10^3 to 1×10^4 cells/well. The following day apoptotic inducers were added at indicated concentrations. Cells were incubated for the indicated time periods (usually 16-30 hours). The next day the medium was removed and cells were stained with 5 $\mu\text{g}/\text{ml}$ Hoechst (Molecular Probes, Inc.) in fresh medium and incubated for 30 minutes at 30°C. Cells were washed in HBSS and fixed with 3.7% formaldehyde in HBSS at room temperature. Plates were washed with HBSS and permeabilized with 0.5% v/v Triton X-100 in HBSS at room temperature. Plates were washed in HBSS and stained with 100 μl of 1U/ml of Alexa 488 Phalloidin stock (100 $\mu\text{l}/\text{well}$, Molecular Probes, Inc.). Cells were washed 2X with HBSS at RT and the plate was sealed.

Quantitation of f-actin content was accomplished by measuring the intensity of phalloidin staining around the nucleus. This was determined to be a reasonable approximation of a full cytoplasmic average of the intensity. The mask used to approximate this cytoplasmic measure was derived from the nuclear mask defined by

the Hoechst stain. Derivation was accomplished by combinations of erosions and dilations.

Results and Discussion

5 Changes in f-actin content varied based on cell type and apoptotic inducer (Fig 27). Staurosporine (30 hours) induced increases in f-actin in L929 (Fig. 27A) and BHK (Fig. 27B) cells. MCF-7 cells exhibited a concentration-dependent response. At low concentrations (Fig. 27E) there appeared to be a decrease in f-actin content. At higher concentrations, f-actin content increased. Paclitaxel (30 hours) treatment led to a wide
10 variety of responses. L929 cells responded with graded increases in f-actin (Fig. 27B) whereas both BHK and MCF-7 responses were highly variable (Figs. 27D & 27F, respectively).

15 **Result of Evaluation:** Both increases and decreases in signal intensity were measured for several cell lines and found to exhibit a concentration dependent response. For certain cell line/apoptotic inducer pairs this could be a statistically significant apoptotic indicator.

Changes in Mitochondrial Mass/Potential

20 Introduction

Changes in mitochondria play a central role in apoptosis (Henkart and Grinstein. 1996. *J Exp Med.* 183:1293-5). Mitochondria release apoptogenic factors through the outer membrane and dissipate the electrochemical gradient of the inner membrane. This is thought to occur via formation of the mitochondria permeability
25 transition (MPT), although it is apparently not true in all cases. An obvious manifestation of the formation of the MPT is collapse of the mitochondrial membrane potential. Inhibition of MPT by pharmacological intervention or mitochondrial expression of the anti-apoptotic protein Bcl-2 prevents cell death, suggesting the formation of the MPT may be a rate-limiting event of the death process (For review see: Kroemer et al. 1998. *Annu Rev Physiol.* 60:619-42). It has also been observed that mitochondria can proliferate during stimulation of apoptosis (Mancini et al. 1997. *J Cell Biol.* 138:449-69; Camilleri-Broet et al. 1998. *Exp Cell Res.* 239:277-92).

One approach for measuring apoptosis-induced changes in mitochondria is to measure the mitochondrial membrane potential. Of the methods available, the simplest measure is the redistribution of a cationic dye that distributes within intracellular organelles based on the membrane potential. Such an approach traditionally requires live cells for the measurements. The recent introduction of the MitoTracker dyes (Poot et al. 1997. *Cytometry*. 27:358-64; available from Molecular Probes, Inc., Oregon) provides a means of measuring mitochondrial membrane potential after fixation.

Given the observations of a possible increase in mitochondrial mass during apoptosis, the amount of dye labeling the mitochondria is related to both membrane potential and the number of mitochondria. If the number of mitochondria remains constant then the amount of dye is directly related to the membrane potential. If the number of mitochondria is not constant, then the signal will likely be dominated by the increase in mass (Reipert et al. 1995. *Exp Cell Res.* 221:281-8).

Probes are available that allow a clear separation between changes in mass and potential in HCS assays. Mitochondrial mass is measured directly by labeling with Mitotracker Green FM (Poot and Pierce, 1999, *Cytometry*. 35:311-7; available from Molecular Probes, Inc., Oregon). The labeling is independent of mitochondrial membrane potential but proportional to mitochondrial mass. This also provides a means of normalizing other mitochondrial measures in each cell with respect to mitochondrial mass.

Material and Methods

Cells were plated into 96-well plates at densities of 3×10^3 to 1×10^4 cells/well. The following day apoptotic inducers were added at the indicated concentrations and cells were incubated for the indicated time periods (usually 16-30 hours). Cells were stained with 5 $\mu\text{g}/\text{ml}$ Hoechst (Molecular Probes, Inc.) and 750 nM MitoTracker Red (CMXRos, Molecular Probes, Inc.) in fresh medium and incubated for 30 minutes at 37°C. Cells were washed in HBSS and fixed with 3.7% formaldehyde in HBSS at room temperature. Plates were washed with HBSS and permeabilized with 0.5% v/v Triton X-100 in HBSS at room temperature. Cells were washed 2X with HBSS at room temperature and the plate was sealed. For dual labeling of mitochondria, cells were

treated with 200 nM Mitotracker Green and 200 nM Mitotracker Red for 0.5 hours before fixation.

Results & Discussion

- 5 Induction of apoptosis by staurosporine and paclitaxel led to varying mitochondrial changes depending upon the stimulus. L929 cells exhibited a clear increase in mitochondrial mass with increasing staurosporine concentrations (Fig. 28). BHK cells exhibited either a decrease in membrane potential at lower concentrations of staurosporine, or an increase in mass at higher concentrations of staurosporine (Fig. 10 28C). MCF-7 cells responded by a consistent decrease in mitochondrial membrane potential in response to increasing concentrations of staurosporine (Fig 28E). Increasing concentrations of paclitaxel caused consistent increases in mitochondrial mass (Fig 28B, 28D, and 28F).

The mitochondrial membrane potential is measured by labeling mitochondria 15 with both Mitotracker Green FM and Mitotracker Red (Molecular Probes, Inc). Mitotracker Red labeling is proportional to both mass and membrane potential. Mitotracker Green FM labeling is proportional to mass. The ratio of Mitotracker Red signal to the Mitotracker Green FM signal provides a measure of mitochondrial membrane potential (Poot and Pierce, 1999). This ratio normalizes the mitochondrial 20 mass with respect to the Mitotracker Red signal. (See Figure 28G) Combining the ability to normalize to mitochondrial mass with a measure of the membrane potential allows independent assessment of both parameters.

- Result of Evaluation: Both decreases in potential and increases in mass were observed
25 depending on the cell line and inducer tested. Dose dependent correlation demonstrates that this is a promising apoptotic indicator.

It is possible to combine multiple measures of apoptosis by exploiting the spectral domain of fluorescence spectroscopy. In fact, all of the nuclear morphology/f-actin content/mitochondrial mass/mitochondrial potential data shown earlier were
30 collected as multiparameter assays, but were presented individually for clarity.

Example 7. Protease induced translocation of a signaling enzyme containing a disease-associated sequence from cytoplasm to nucleus.

Plasmid construct. A eukaryotic expression plasmid containing a coding sequence for a green fluorescent protein – caspase (Cohen (1997), *Biochemical J.* 326:1-16; Liang et al. (1997), *J. of Molec. Biol.* 274:291-302) chimera is prepared using GFP mutants. The construct is used to transfect eukaryotic cells.

Cell preparation and transfection. Cells are trypsinized and plated 24 h prior to transfection and incubated at 37°C and 5% CO₂. Transfections are performed by methods including, but not limited to calcium phosphate coprecipitation or lipofection. Cells are incubated with the calcium phosphate-DNA precipitate for 4-5 hours at 37°C and 5% CO₂, washed 3-4 times with DMEM to remove the precipitate, followed by the addition of C-DMEM. Lipofectamine transfections are performed in serum-free DMEM without antibiotics according to the manufacturer's instructions. Following a 2-3 hour incubation with the DNA-liposome complexes, the medium is removed and replaced with C-DMEM.

Apoptotic induction of Caspase-GFP translocation. To obtain Caspase-GFP translocation kinetic data, nuclei of transfected cells are first labeled with 5 µg/ml Hoechst 33342 (Molecular Probes) in C-DMEM for 20 minutes at 37°C and 5% CO₂. Cells are washed once in Hank's Balanced Salt Solution (HBSS) followed by the addition of compounds that induce apoptosis. These compounds include, but are not limited to paclitaxel, staurosporine, ceramide, and tumor necrosis factor. To obtain fixed time point titration data, transfected cells are first washed with DMEM and then incubated at 37°C and 5% CO₂ for 1 h in the presence of 0 – 1000 nM compound in DMEM. Cells are analyzed live or they are rinsed with HBSS, fixed for 15 min with 3.7% formaldehyde in HBSS, stained with Hoechst 33342, and washed before analysis.

Image acquisition and analysis. Kinetic data are collected by acquiring fluorescence image pairs (Caspase-GFP and Hoechst 33342-labeled nuclei) from fields of living cells at 1 min intervals for 30 min after the addition of compound. Likewise, image pairs are obtained from each well of the fixed time point screening plates 1 h after the addition of compound. In both cases, the image pairs obtained at each time point are used to define nuclear and cytoplasmic regions in each cell. Translocation of

Caspase-GFP is calculated by dividing the integrated fluorescence intensity of Caspase-GFP in the nucleus by the integrated fluorescence intensity of the chimera in the cytoplasm or as a nuclear-cytoplasmic difference of GFP fluorescence. In the fixed time point screen this translocation ratio is calculated from data obtained from at least 5 200 cells at each concentration of compound tested. Drug-induced translocation of Caspase-GFP from the cytoplasm to the nucleus is therefore correlated with an increase in the translocation ratio. Molecular interaction libraries including, but not limited to those comprising putative activators or inhibitors of apoptosis-activated enzymes are used to screen the indicator cell lines and identify a specific ligand for the DAS, and a 10 pathway activated by compound activity.

Example 8. Identification of novel steroid receptors from DAS

Two sources of material and/or information are required to make use of this embodiment, which allows assessment of the function of an uncharacterized gene. 15 First, disease associated sequence bank(s) containing cDNA sequences suitable for transfection into mammalian cells can be used. Because every RADE or differential expression experiment generates up to several hundred sequences, it is possible to generate an ample supply of DAS. Second, information from primary sequence database searches can be used to place DAS into broad categories, including, but not 20 limited to, those that contain signal sequences, seven trans-membrane motifs, conserved protease active site domains, or other identifiable motifs. Based on the information acquired from these sources, method types and indicator cell lines to be transfected are selected. A large number of motifs are already well characterized and encoded in the linear sequences contained within the large number genes in existing 25 genomic databases.

In one embodiment, the following steps are taken:

- 1) Information from the DAS identification experiment (including database searches) is used as the basis for selecting the relevant biological processes. (for example, look at the DAS from a tumor line for cell cycle modulation, apoptosis, metastatic proteases, etc.) 30
- 2) Sorting of DNA sequences or DAS by identifiable motifs (ie. signal sequences, 7-transmembrane domains, conserved protease active site domains, etc.) This initial grouping will determine fluorescent tagging strategies, host cell lines,

indicator cell lines, and banks of bioactive molecules to be screened, as described *supra*.

5 3) Using well established molecular biology methods, ligate DAS into an expression vector designed for this purpose. Generalized expression vectors contain promoters, enhancers, and terminators for which to deliver target sequences to the cell for transient expression. Such vectors may also contain antibody tagging sequences, direct association sequences, chromophore fusion sequences like GFP, etc. to facilitate detection when expressed by the host.

10 4) Transiently transfet cells with DAS containing vectors using standard transfection protocols including: calcium phosphate co-precipitation, liposome mediated, DEAE dextran mediated, polycationic mediated, viral mediated, or electroporation, and plate into microtiter plates or microwell arrays. Alternatively, transfection can be done directly in the microtiter plate itself.

15 5) Carry out the cell screening methods as described *supra*.

In this embodiment, DAS shown to possess a motif(s) suggestive of transcriptional activation potential (for example, DNA binding domain, amino terminal modulating domain, hinge region, or carboxy terminal ligand binding domain) are utilized to identify novel steroid receptors.

20 Defining the fluorescent tags for this experiment involves identification of the nucleus through staining, and tagging the DAS by creating a GFP chimera via insertion of DAS into an expression vector, proximally fused to the gene encoding GFP. Alternatively, a single chain antibody fragment with high affinity to some portion of the expressed DAS could be constructed using technology available in the art (Cambridge

25 Antibody Technologies) and linked to a fluorophore (FITC) to tag the putative transcriptional activator/receptor in the cells. This alternative would provide an external tag requiring no DNA transfection and therefore would be useful if distribution data were to be gathered from the original primary cultures used to generate the DAS.

30 *Plasmid construct.* A eukaryotic expression plasmid containing a coding sequence for a green fluorescent protein - DAS chimera is prepared using GFP mutants. The construct is used to transfect HeLa cells. The plasmid, when transfected into the host cell, produces a GFP fused to the DAS protein product, designated GFP-DASpp.

Cell preparation and transfection. HeLa cells are trypsinized and plated using DMEM containing 5% charcoal/dextran-treated fetal bovine serum (FBS) (Hyclone) and 1% penicillin-streptomycin (C-DMEM) 12-24 hours prior to transfection and incubated at 37°C and 5% CO₂. Transfections are performed by calcium phosphate coprecipitation or with Lipofectamine (Life Technologies). For the calcium phosphate transfections, the medium is replaced, prior to transfection, with DMEM containing 5% charcoal/dextran-treated FBS. Cells are incubated with the calcium phosphate-DNA precipitate for 4-5 hours at 37°C and 5% CO₂, and washed 3-4 times with DMEM to remove the precipitate, followed by the addition of C-DMEM. Lipofectamine transfections are performed in serum-free DMEM without antibiotics according to the manufacturer's instructions. Following a 2-3 hour incubation with the DNA-liposome complexes, the medium is removed and replaced with C-DMEM. All transfected cells in 96-well microtiter plates are incubated at 33°C and 5% CO₂ for 24-48 hours prior to drug treatment. Experiments are performed with the receptor expressed transiently in HeLa cells.

Localization of expressed GFP-DASpp inside cells. To obtain cellular distribution data, nuclei of transfected cells are first labeled with 5 µg/ml Hoechst 33342 (Molecular Probes) in C-DMEM for 20 minutes at 33°C and 5% CO₂. Cells are washed once in Hank's Balanced Salt Solution (HBSS). The cells are analyzed live or they are rinsed with HBSS, fixed for 15 min with 3.7% formaldehyde in HBSS, stained with Hoechst 33342, and washed before analysis.

In a preferred embodiment, image acquisition and analysis are performed using the cell screening system of the present invention. The intracellular GFP-DASpp fluorescence signal is collected by acquiring fluorescence image pairs (GFP-DASpp and Hoechst 33342-labeled nuclei) from field cells. The image pairs obtained at each time point are used to define nuclear and cytoplasmic regions in each cell. Data demonstrating dispersed signal in the cytoplasm would be consistent with known steroid receptors that are DNA transcriptional activators.

Screening for induction of GFP-DASpp translocation. Using the above construct, confirmed for appropriate expression of the GFP-DASpp, as an indicator cell line, a screen of various ligands is performed using a series of steroid type ligands including, but not limited to: estrogen, progesterone, retinoids, growth factors,

androgens, and many other steroid and steroid based molecules. Image acquisition and analysis are performed using the cell screening system of the invention. The intracellular GFP-DASpp fluorescence signal is collected by acquiring fluorescence image pairs (GFP-DASpp and Hoechst 33342-labeled nuclei) from fields cells. The 5 image pairs obtained at each time point are used to define nuclear and cytoplasmic regions in each cell. Translocation of GFP-DASpp is calculated by dividing the integrated fluorescence intensity of GFP-DASpp in the nucleus by the integrated fluorescence intensity of the chimera in the cytoplasm or as a nuclear-cytoplasmic difference of GFP fluorescence. A translocation from the cytoplasm into the nucleus 10 indicates a ligand binding activation of the DASpp thus identifying the potential receptor class and action. Combining this data with other data obtained in a similar fashion using known inhibitors and modifiers of steroid receptors, would either validate the DASpp as a target, or more data would be generated from various sources.

15 **Example 9 Additional Screens**

Translocation between the plasma membrane and the cytoplasm:

Profilactin complex dissociation and binding of profilin to the plasma membrane. In one embodiment, a fluorescent protein biosensor of profilin membrane binding is prepared by labeling purified profilin (Federov et al.(1994), *J. Molec. Biol.* 241:480-482; Lanbrechts et al. (1995), *Eur. J. Biochem.* 230:281-286) with a probe possessing a fluorescence lifetime in the range of 2-300 ns. The labeled profilin is introduced into living indicator cells using bulk loading methodology and the indicator cells are treated with test compounds. Fluorescence anisotropy imaging microscopy (Gough and Taylor (1993), *J. Cell Biol.* 121:1095-1107) is used to measure test- 20 compound dependent movement of the fluorescent derivative of profilin between the cytoplasm and membrane for a period of time after treatment ranging from 0.1 s to 10 h.

Rho-RhoGDI complex translocation to the membrane. In another embodiment, indicator cells are treated with test compounds and then fixed, washed, 30 and permeabilized. The indicator cell plasma membrane, cytoplasm, and nucleus are all labeled with distinctly colored markers followed by immunolocalization of Rho protein (Self et al. (1995), *Methods in Enzymology* 256:3-10; Tanaka et al. (1995),

Methods in Enzymology 256:41-49) with antibodies labeled with a fourth color. Each of the four labels is imaged separately using the cell screening system, and the images used to calculate the amount of inhibition or activation of translocation effected by the test compound. To do this calculation, the images of the probes used to mark the

5 plasma membrane and cytoplasm are used to mask the image of the immunological probe marking the location of intracellular Rho protein. The integrated brightness per unit area under each mask is used to form a translocation quotient by dividing the plasma membrane integrated brightness/area by the cytoplasmic integrated brightness/area. By comparing the translocation quotient values from control and

10 experimental wells, the percent translocation is calculated for each potential lead compound.

β-Arrestin translocation to the plasma membrane upon G-protein receptor activation.

In another embodiment of a cytoplasm to membrane translocation high-content screen, the translocation of β-arrestin protein from the cytoplasm to the plasma membrane is measured in response to cell treatment. To measure the translocation, living indicator cells containing luminescent domain markers are treated with test compounds and the movement of the β-arrestin marker is measured in time and space using the cell screening system of the present invention. In a preferred embodiment, the indicator cells contain luminescent markers consisting of a green fluorescent protein β-arrestin (GFP-β-arrestin) protein chimera (Barak et al. (1997), *J. Biol. Chem.* 272:27497-27500; Daaka et al. (1998), *J. Biol. Chem.* 273:685-688) that is expressed by the indicator cells through the use of transient or stable cell transfection and other reporters used to mark cytoplasmic and membrane domains. When the indicator cells are in the resting state, the domain marker molecules partition predominately in the plasma membrane or in the cytoplasm. In the high-content screen, these markers are used to delineate the cell cytoplasm and plasma membrane in distinct channels of fluorescence. When the indicator cells are treated with a test compound, the dynamic redistribution of the GFP-β-arrestin is recorded as a series of images over a time scale ranging from 0.1 s to 10 h. In a preferred embodiment, the time scale is 1 h. Each image is analyzed by a method that quantifies the movement of the GFP-β-arrestin

protein chimera between the plasma membrane and the cytoplasm. To do this calculation, the images of the probes used to mark the plasma membrane and cytoplasm are used to mask the image of the GFP- β -arrestin probe marking the location of intracellular GFP- β -arrestin protein. The integrated brightness per unit area under each
5 mask is used to form a translocation quotient by dividing the plasma membrane integrated brightness/area by the cytoplasmic integrated brightness/area. By comparing the translocation quotient values from control and experimental wells, the percent translocation is calculated for each potential lead compound. The output of the high-content screen relates quantitative data describing the magnitude of the translocation
10 within a large number of individual cells that have been treated with test compounds of interest.

Translocation between the endoplasmic reticulum and the Golgi:

In one embodiment of an endoplasmic reticulum to Golgi translocation high-content screen, the translocation of a VSVG protein from the ts045 mutant strain of vesicular stomatitis virus (Ellenberg et al. (1997), *J. Cell Biol.* 138:1193-1206; Presley et al. (1997) *Nature* 389:81-85) from the endoplasmic reticulum to the Golgi domain is measured in response to cell treatment. To measure the translocation, indicator cells containing luminescent reporters are treated with test compounds and the movement of the reporters is measured in space and time using the cell screening system of the
20 present invention. The indicator cells contain luminescent reporters consisting of a GFP-VSVG protein chimera that is expressed by the indicator cell through the use of transient or stable cell transfection and other domain markers used to measure the localization of the endoplasmic reticulum and Golgi domains. When the indicator cells are in their resting state at 40°C, the GFP-VSVG protein chimera molecules are
25 partitioned predominately in the endoplasmic reticulum. In this high-content screen, domain markers of distinct colors used to delineate the endoplasmic reticulum and the Golgi domains in distinct channels of fluorescence. When the indicator cells are treated with a test compound and the temperature is simultaneously lowered to 32°C, the dynamic redistribution of the GFP-VSVG protein chimera is recorded as a series of
30 images over a time scale ranging from 0.1 s to 10 h. Each image is analyzed by a method that quantifies the movement of the GFP-VSVG protein chimera between the endoplasmic reticulum and the Golgi domains. To do this calculation, the images of

the probes used to mark the endoplasmic reticulum and the Golgi domains are used to mask the image of the GFP-VSVG probe marking the location of intracellular GFP-VSVG protein. The integrated brightness per unit area under each mask is used to form a translocation quotient by dividing the endoplasmic reticulum integrated brightness/area by the Golgi integrated brightness/area. By comparing the translocation quotient values from control and experimental wells, the percent translocation is calculated for each potential lead compound. The output of the high-content screen relates quantitative data describing the magnitude of the translocation within a large number of individual cells that have been treated with test compounds of interest at final concentrations ranging from 10^{-12} M to 10^{-3} M for a period ranging from 1 min to 10 h.

Induction and inhibition of organellar function:

Intracellular microtubule stability.

15 In another aspect of the invention, an automated method for identifying compounds that modify microtubule structure is provided. In this embodiment, indicator cells are treated with test compounds and the distribution of luminescent microtubule-labeling molecules is measured in space and time using a cell screening system, such as the one disclosed above. The luminescent microtubule-labeling molecules may be expressed by or added to the cells either before, together with, or after contacting the cells with a test compound.

20 In one embodiment of this aspect of the invention, living cells express a luminescently labeled protein biosensor of microtubule dynamics, comprising a protein that labels microtubules fused to a luminescent protein. Appropriate microtubule-labeling proteins for this aspect of the invention include, but are not limited to α and β tubulin isoforms, and MAP4. Preferred embodiments of the luminescent protein include, but are not limited to green fluorescent protein (GFP) and GFP mutants. In a preferred embodiment, the method involves transfecting cells with a microtubule labeling luminescent protein, wherein the microtubule labeling protein can be, but is not limited to, α -tubulin, β -tubulin, or microtubule-associated protein 4 (MAP4). The approach outlined here enables those skilled in the art to make live cell measurements

to determine the effect of lead compounds on tubulin activity and microtubule stability *in vivo*.

In a most preferred embodiment, MAP4 is fused to a modified version of the *Aequorea victoria* green fluorescent protein (GFP). A DNA construct has been made
5 which consists of a fusion between the EGFP coding sequence (available from Clontech) and the coding sequence for mouse MAP4. (Olson et al., (1995), J. Cell Biol. 130(3): 639-650). MAP4 is a ubiquitous microtubule-associated protein that is known to interact with microtubules in interphase as well as mitotic cells (Olmsted and Murofushi, (1993), MAP4. In "Guidebook to the Cytoskeleton and Motor Proteins."
10 Oxford University Press. T. Kreis and R. Vale, eds.) Its localization, then, can serve as an indicator of the localization, organization, and integrity of microtubules in living (or fixed) cells at all stages of the cell cycle for cell-based HCS assays. While MAP2 and tau (microtubule associated proteins expressed specifically in neuronal cells) have been used to form GFP chimeras (Kaech et al., (1996) Neuron. 17: 1189-1199; Hall et al.,
15 (1997), Proc. Nat. Acad. Sci. 94: 4733-4738) their restricted cell type distribution and the tendency of these proteins to bundle microtubules when overexpressed make these proteins less desirable as molecular reagents for analysis in live cells originating from varied tissues and organs. Moderate overexpression of GFP-MAP4 does not disrupt microtubule function or integrity (Olson et al., 1995). Similar constructs can be made
20 using β -tubulin or α -tubulin via standard techniques in the art. These chimeras will provide a means to observe and analyze microtubule activity in living cells during all stages of the cell cycle.

In another embodiment, the luminescently labeled protein biosensor of microtubule dynamics is expressed, isolated, and added to the cells to be analyzed via
25 bulk loading techniques, such as microinjection, scrape loading, and impact-mediated loading. In this embodiment, there is not an issue of overexpression within the cell, and thus α and β tubulin isoforms, MAP4, MAP2 and/or tau can all be used.

In a further embodiment, the protein biosensor is expressed by the cell, and the cell is subsequently contacted with a luminescent label, such as a labeled antibody, that
30 detects the protein biosensor, endogenous levels of a protein antigen, or both. In this embodiment, a luminescent label that detects α and β tubulin isoforms, MAP4, MAP2 and/or tau, can be used.

A variety of GFP mutants are available, all of which would be effective in this invention, including, but not limited to, GFP mutants which are commercially available (Clontech, California).

The MAP4 construct has been introduced into several mammalian cell lines
5 (BHK-21, Swiss 3T3, HeLa, HEK 293, LLCPK) and the organization and localization
of tubulin has been visualized in live cells by virtue of the GFP fluorescence as an
indicator of MAP4 localization. The construct can be expressed transiently or stable
cell lines can be prepared by standard methods. Stable HeLa cell lines expressing the
EGFP-MAP4 chimera have been obtained, indicating that expression of the chimera is
10 not toxic and does not interfere with mitosis.

Possible selectable markers for establishment and maintenance of stable cell
lines include, but are not limited to the neomycin resistance gene, hygromycin
resistance gene, zeocin resistance gene, puromycin resistance gene, bleomycin
resistance gene, and blastacidin resistance gene.

15 The utility of this method for the monitoring of microtubule assembly,
disassembly, and rearrangement has been demonstrated by treatment of transiently and
stably transfected cells with microtubule drugs such as paclitaxel, nocodazole,
vincristine, or vinblastine.

20 The present method provides high-content and combined high throughput-high
content cell-based screens for anti-microtubule drugs, particularly as one parameter in a
multi-parametric cancer target screen. The EGFP-MAP4 construct used herein can also
be used as one of the components of a high-content screen that measures multiple
signaling pathways or physiological events. In a preferred embodiment, a combined
high throughput and high content screen is employed, wherein multiple cells in each of
25 the locations containing cells are analyzed in a high throughput mode, and only a subset
of the locations containing cells are analyzed in a high content mode. The high
throughput screen can be any screen that would be useful to identify those locations
containing cells that should be further analyzed, including, but not limited to,
identifying locations with increased luminescence intensity, those exhibiting
30 expression of a reporter gene, those undergoing calcium changes, and those
undergoing pH changes.

In addition to drug screening applications, the present invention may be applied to clinical diagnostics, the detection of chemical and biological warfare weapons, and the basic research market since fundamental cell processes, such as cell division and motility, are highly dependent upon microtubule dynamics.

5

Image Acquisition and Analysis

Image data can be obtained from either fixed or living indicator cells. To extract morphometric data from each of the images obtained the following method of analysis is used:

- 10 1. Threshold each nucleus and cytoplasmic image to produce a mask that has value = 0 for each pixel outside a nucleus or cell boundary.
2. Overlay the mask on the original image, detect each object in the field (*i.e.*, nucleus or cell), and calculate its size, shape, and integrated intensity.
3. Overlay the whole cell mask obtained above on the corresponding luminescent microtubule image and apply one or more of the following set of classifiers to determine the microtubule morphology and the effect of drugs on microtubule morphology.

15 Microtubule morphology is defined using a set of classifiers to quantify aspects of microtubule shape, size, aggregation state, and polymerization state. These classifiers can be based on approaches that include co-occurrence matrices, texture measurements, spectral methods, structural methods, wavelet transforms, statistical methods, or combinations thereof. Examples of such classifiers are as follows:

- 20 1. A classifier to quantify microtubule length and width using edge detection methods such as that discussed in Kolega et al. ((1993). *BioImaging* 1:136-150), which discloses a non-automated method to determine edge strength in individual cells, to calculate the total edge strength within each cell. To normalize for cell size, the total edge strength can be divided by the cell area to give a "microtubule morphology" value. Large microtubule morphology values are associated with strong edge strength values and are therefore maximal in cells containing distinct microtubule structures. Likewise, small microtubule morphology values are associated with weak edge strength and are minimal in cells with depolymerized microtubules. The physiological range of microtubule morphology values is set by treating cells with either the microtubule stabilizing drug paclitaxel (10 μ M) or the microtubule depolymerizing drug nocodazole (10 μ g/ml).
- 25 2. A classifier to quantify microtubule aggregation into punctate spots or foci using methodology from the receptor internalization methods discussed supra.

35

3. A classifier to quantify microtubule depolymerization using a measure of image texture.

5 4. A classifier to quantify apparent interconnectivity, or branching (or both), of the microtubules.

10 5. Measurement of the kinetics of microtubule reorganization using the above classifiers on a time series of images of cells treated with test compounds.

In a further aspect, kits are provided for analyzing microtubule stability, comprising an expression vector comprising a nucleic acid that encodes a microtubule labeling protein and instructions for using the expression vector for carrying out the methods described above. In a preferred embodiment, the expression vector further comprises a nucleic acid that encodes a luminescent protein, wherein the microtubule binding protein and the luminescent protein thereof are expressed as a fusion protein. Alternatively, the kit may contain an antibody that specifically binds to the microtubule-labeling protein. In a further embodiment, the kit includes cells that express the microtubule labeling protein. In a preferred embodiment, the cells are transfected with the expression vector. In another preferred embodiment, the kits further contain a compound that is known to disrupt microtubule structure, including but not limited to curacin, nocodazole, vincristine, or vinblastine. In another preferred embodiment, the kits further comprise a compound that is known to stabilize microtubule structure, including but not limited to taxol (paclitaxel), and discodermolide.

In another aspect, the present invention comprises a machine readable storage medium comprising a program containing a set of instructions for causing a cell screening system to execute the disclosed methods for analyzing microtubule stability, wherein the cell screening system comprises an optical system with a stage adapted for holding a plate containing cells, a digital camera, a means for directing fluorescence or luminescence emitted from the cells to the digital camera, and a computer means for receiving and processing the digital data from the digital camera.

High-content screens involving the functional localization of macromolecules

Within this class of high-content screen, the functional localization of macromolecules in response to external stimuli is measured within living cells.

5 **Glycolytic enzyme activity regulation.** In a preferred embodiment of a cellular enzyme activity high-content screen, the activity of key glycolytic regulatory enzymes are measured in treated cells. To measure enzyme activity, indicator cells containing luminescent labeling reagents are treated with test compounds and the activity of the reporters is measured in space and time using cell screening system of the present invention.

10 In one embodiment, the reporter of intracellular enzyme activity is fructose-6-phosphate, 2-kinase/fructose-2,6-bisphosphatase (PFK-2), a regulatory enzyme whose phosphorylation state indicates intracellular carbohydrate anabolism or catabolism (Deprez et al. (1997) *J. Biol. Chem.* 272:17269-17275; Kealer et al. (1996) *FEBS Letters* 395:225-227; Lee et al. (1996), *Biochemistry* 35:6010-6019). The indicator 15 cells contain luminescent reporters consisting of a fluorescent protein biosensor of PFK-2 phosphorylation. The fluorescent protein biosensor is constructed by introducing an environmentally sensitive fluorescent dye near to the known phosphorylation site of the enzyme (Deprez et al. (1997), *supra*; Giuliano et al. (1995), *supra*). The dye can be of the ketocyanine class (Kessler and Wolfbeis (1991), 20 *Spectrochimica Acta* 47A:187-192) or any class that contains a protein reactive moiety and a fluorochrome whose excitation or emission spectrum is sensitive to solution polarity. The fluorescent protein biosensor is introduced into the indicator cells using bulk loading methodology.

Living indicator cells are treated with test compounds, at final concentrations 25 ranging from 10^{-12} M to 10^3 M for times ranging from 0.1 s to 10 h. In a preferred embodiment, ratio image data are obtained from living treated indicator cells by collecting a spectral pair of fluorescence images at each time point. To extract morphometric data from each time point, a ratio is made between each pair of images by numerically dividing the two spectral images at each time point, pixel by pixel. 30 Each pixel value is then used to calculate the fractional phosphorylation of PFK-2. At small fractional values of phosphorylation, PFK-2 stimulates carbohydrate catabolism.

At high fractional values of phosphorylation, PFK-2 stimulates carbohydrate anabolism.

5 **Protein kinase A activity and localization of subunits.** In another embodiment of a high-content screen, both the domain localization and activity of protein kinase A (PKA) within indicator cells are measured in response to treatment with test compounds.

10 The indicator cells contain luminescent reporters including a fluorescent protein biosensor of PKA activation. The fluorescent protein biosensor is constructed by introducing an environmentally sensitive fluorescent dye into the catalytic subunit of PKA near the site known to interact with the regulatory subunit of PKA (Harootunian et al. (1993), *Mol. Biol. of the Cell* 4:993-1002; Johnson et al. (1996), *Cell* 85:149-158; Giuliano et al. (1995), *supra*). The dye can be of the ketocyanine class (Kessler, and Wolfbeis (1991), *Spectrochimica Acta* 47A:187-192) or any class that contains a 15 protein reactive moiety and a fluorochrome whose excitation or emission spectrum is sensitive to solution polarity. The fluorescent protein biosensor of PKA activation is introduced into the indicator cells using bulk loading methodology.

In one embodiment, living indicator cells are treated with test compounds, at final concentrations ranging from 10^{-12} M to 10^{-3} M for times ranging from 0.1 s to 10 h. In a preferred embodiment, ratio image data are obtained from living treated indicator cells. To extract biosensor data from each time point, a ratio is made between each pair of images, and each pixel value is then used to calculate the fractional activation of PKA (e.g., separation of the catalytic and regulatory subunits after cAMP binding). At high fractional values of activity, PFK-2 stimulates biochemical cascades 25 within the living cell.

To measure the translocation of the catalytic subunit of PKA, indicator cells containing luminescent reporters are treated with test compounds and the movement of the reporters is measured in space and time using the cell screening system. The indicator cells contain luminescent reporters consisting of domain markers used to 30 measure the localization of the cytoplasmic and nuclear domains. When the indicator cells are treated with a test compounds, the dynamic redistribution of a PKA fluorescent protein biosensor is recorded intracellularly as a series of images over a

time scale ranging from 0.1 s to 10 h. Each image is analyzed by a method that quantifies the movement of the PKA between the cytoplasmic and nuclear domains. To do this calculation, the images of the probes used to mark the cytoplasmic and nuclear domains are used to mask the image of the PKA fluorescent protein biosensor. The 5 integrated brightness per unit area under each mask is used to form a translocation quotient by dividing the cytoplasmic integrated brightness/area by the nuclear integrated brightness/area. By comparing the translocation quotient values from control and experimental wells, the percent translocation is calculated for each potential lead compound. The output of the high-content screen relates quantitative data 10 describing the magnitude of the translocation within a large number of individual cells that have been treated with test compound in the concentration range of 10^{-12} M to 10^{-3} M.

High-content screens involving the induction or inhibition of gene expression

15 *RNA-based fluorescent biosensors*

Cytoskeletal protein transcription and message localization. Regulation of the general classes of cell physiological responses including cell-substrate adhesion, cell-cell adhesion, signal transduction, cell-cycle events, intermediary and signaling molecule metabolism, cell locomotion, cell-cell communication, and cell death can 20 involve the alteration of gene expression. High-content screens can also be designed to measure this class of physiological response.

In one embodiment, the reporter of intracellular gene expression is an oligonucleotide that can hybridize with the target mRNA and alter its fluorescence signal. In a preferred embodiment, the oligonucleotide is a molecular beacon (Tyagi 25 and Kramer (1996) *Nat. Biotechnol.* 14:303-308), a luminescence-based reagent whose fluorescence signal is dependent on intermolecular and intramolecular interactions. The fluorescent biosensor is constructed by introducing a fluorescence energy transfer pair of fluorescent dyes such that there is one at each end (5' and 3') of the reagent. The dyes can be of any class that contains a protein reactive moiety and fluorochromes 30 whose excitation and emission spectra overlap sufficiently to provide fluorescence energy transfer between the dyes in the resting state, including, but not limited to, fluorescein and rhodamine (Molecular Probes, Inc.). In a preferred embodiment, a

portion of the message coding for β -actin (Kislaukis et al. (1994), *J. Cell Biol.* 127:441-451; McCann et al. (1997), *Proc. Natl. Acad. Sci.* 94:5679-5684; Sutoh (1982), *Biochemistry* 21:3654-3661) is inserted into the loop region of a hairpin-shaped oligonucleotide with the ends tethered together due to intramolecular hybridization. At 5 each end of the biosensor a fluorescence donor (fluorescein) and a fluorescence acceptor (rhodamine) are covalently bound. In the tethered state, the fluorescence energy transfer is maximal and therefore indicative of an unhybridized molecule. When hybridized with the mRNA coding for β -actin, the tether is broken and energy transfer is lost. The complete fluorescent biosensor is introduced into the indicator 10 cells using bulk loading methodology.

In one embodiment, living indicator cells are treated with test compounds, at final concentrations ranging from 10^{-12} M to 10^{-3} M for times ranging from 0.1 s to 10 h. In a preferred embodiment, ratio image data are obtained from living treated indicator cells. To extract morphometric data from each time point, a ratio is made 15 between each pair of images, and each pixel value is then used to calculate the fractional hybridization of the labeled nucleotide. At small fractional values of hybridization little expression of β -actin is indicated. At high fractional values of hybridization, maximal expression of β -actin is indicated. Furthermore, the distribution of hybridized molecules within the cytoplasm of the indicator cells is also a measure of 20 the physiological response of the indicator cells.

Cell surface binding of a ligand

Labeled insulin binding to its cell surface receptor in living cells. Cells whose plasma membrane domain has been labeled with a labeling reagent of a particular color are incubated with a solution containing insulin molecules (Lee et al. 25 (1997), *Biochemistry* 36:2701-2708; Martinez-Zaguilan et al. (1996), *Am. J. Physiol.* 270:C1438-C1446) that are labeled with a luminescent probe of a different color for an appropriate time under the appropriate conditions. After incubation, unbound insulin molecules are washed away, the cells fixed and the distribution and concentration of the 30 insulin on the plasma membrane is measured. To do this, the cell membrane image is used as a mask for the insulin image. The integrated intensity from the masked insulin image is compared to a set of images containing known amounts of labeled insulin.

The amount of insulin bound to the cell is determined from the standards and used in conjunction with the total concentration of insulin incubated with the cell to calculate a dissociation constant or insulin to its cell surface receptor.

5 *Labeling of cellular compartments*

Whole cell labeling

Whole cell labeling is accomplished by labeling cellular components such that dynamics of cell shape and motility of the cell can be measured over time by analyzing fluorescence images of cells.

10 In one embodiment, small reactive fluorescent molecules are introduced into living cells. These membrane-permeant molecules both diffuse through and react with protein components in the plasma membrane. Dye molecules react with intracellular molecules to both increase the fluorescence signal emitted from each molecule and to entrap the fluorescent dye within living cells. These molecules include reactive
15 chloromethyl derivatives of aminocoumarins, hydroxycoumarins, eosin diacetate, fluorescein diacetate, some Bodipy dye derivatives, and tetramethylrhodamine. The reactivity of these dyes toward macromolecules includes free primary amino groups and free sulphydryl groups.

20 In another embodiment, the cell surface is labeled by allowing the cell to interact with fluorescently labeled antibodies or lectins (Sigma Chemical Company, St. Louis, MO) that react specifically with molecules on the cell surface. Cell surface protein chimeras expressed by the cell of interest that contain a green fluorescent protein, or mutant thereof, component can also be used to fluorescently label the entire cell surface. Once the entire cell is labeled, images of the entire cell or cell array can
25 become a parameter in high content screens, involving the measurement of cell shape, motility, size, and growth and division.

Plasma membrane labeling

30 In one embodiment, labeling the whole plasma membrane employs some of the same methodology described above for labeling the entire cells. Luminescent molecules that label the entire cell surface act to delineate the plasma membrane.

In a second embodiment subdomains of the plasma membrane, the extracellular surface, the lipid bilayer, and the intracellular surface can be labeled separately and used as components of high content screens. In the first embodiment, the extracellular surface is labeled using a brief treatment with a reactive fluorescent molecule such as
5 the succinimidyl ester or iodoacetamide derivatives of fluorescent dyes such as the fluoresceins, rhodamines, cyanines, and Bodipys.

In a third embodiment, the extracellular surface is labeled using fluorescently labeled macromolecules with a high affinity for cell surface molecules. These include fluorescently labeled lectins such as the fluorescein, rhodamine, and cyanine
10 derivatives of lectins derived from jack bean (Con A), red kidney bean (erythroagglutinin PHA-E), or wheat germ.

In a fourth embodiment, fluorescently labeled antibodies with a high affinity for cell surface components are used to label the extracellular region of the plasma membrane. Extracellular regions of cell surface receptors and ion channels are
15 examples of proteins that can be labeled with antibodies.

In a fifth embodiment, the lipid bilayer of the plasma membrane is labeled with fluorescent molecules. These molecules include fluorescent dyes attached to long chain hydrophobic molecules that interact strongly with the hydrophobic region in the center of the plasma membrane lipid bilayer. Examples of these dyes include the PKH series
20 of dyes (U.S. 4,783,401, 4,762701, and 4,859,584; available commercially from Sigma Chemical Company, St. Louis, MO), fluorescent phospholipids such as nitrobenzoxadiazole glycerophosphoethanolamine and fluorescein-derivatized dihexadecanoylglycerophosphoethanolamine, fluorescent fatty acids such as 5-butyl-4,4-difluoro-4-bora-3a,4a-diaza-s-indacene-3-nonanoic acid and 1-pyrenedecanoic acid
25 (Molecular Probes, Inc.), fluorescent sterols including cholesteryl 4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene-3-dodecanoate and cholesteryl 1-pyrenehexanoate, and fluorescently labeled proteins that interact specifically with lipid bilayer components such as the fluorescein derivative of annexin V (Caltag Antibody Co, Burlingame, CA).

30 In another embodiment, the intracellular component of the plasma membrane is labeled with fluorescent molecules. Examples of these molecules are the intracellular components of the trimeric G-protein receptor, adenylyl cyclase, and ionic transport

proteins. These molecules can be labeled as a result of tight binding to a fluorescently labeled specific antibody or by the incorporation of a fluorescent protein chimera that is comprised of a membrane-associated protein and the green fluorescent protein, and mutants thereof.

5

Endosome fluorescence labeling

In one embodiment, ligands that are transported into cells by receptor-mediated endocytosis are used to trace the dynamics of endosomal organelles. Examples of labeled ligands include Bodipy FL-labeled low density lipoprotein complexes, 10 tetramethylrhodamine transferrin analogs, and fluorescently labeled epidermal growth factor (Molecular Probes, Inc.)

In a second embodiment, fluorescently labeled primary or secondary antibodies (Sigma Chemical Co. St. Louis, MO; Molecular Probes, Inc. Eugene, OR; Caltag Antibody Co.) that specifically label endosomal ligands are used to mark the 15 endosomal compartment in cells.

In a third embodiment, endosomes are fluorescently labeled in cells expressing protein chimeras formed by fusing a green fluorescent protein, or mutants thereof, with a receptor whose internalization labels endosomes. Chimeras of the EGF, transferrin, and low density lipoprotein receptors are examples of these molecules.

20

Lysosome labeling

In one embodiment, membrane permeant lysosome-specific luminescent reagents are used to label the lysosomal compartment of living and fixed cells. These reagents include the luminescent molecules neutral red, N-(3-((2,4-dinitrophenyl)amino)propyl)-N-(3-aminopropyl)methylamine, and the LysoTracker probes which report intralysosomal pH as well as the dynamic distribution of lysosomes (Molecular Probes, Inc.)

In a second embodiment, antibodies against lysosomal antigens (Sigma Chemical Co.; Molecular Probes, Inc.; Caltag Antibody Co.) are used to label 30 lysosomal components that are localized in specific lysosomal domains. Examples of these components are the degradative enzymes involved in cholesterol ester hydrolysis,

membrane protein proteases, and nucleases as well as the ATP-driven lysosomal proton pump.

In a third embodiment, protein chimeras consisting of a lysosomal protein genetically fused to an intrinsically luminescent protein such as the green fluorescent

- 5 protein, or mutants thereof, are used to label the lysosomal domain. Examples of these components are the degradative enzymes involved in cholesterol ester hydrolysis, membrane protein proteases, and nucleases as well as the ATP-driven lysosomal proton pump.

10 **Cytoplasmic fluorescence labeling**

In one embodiment, cell permeant fluorescent dyes (Molecular Probes, Inc.) with a reactive group are reacted with living cells. Reactive dyes including monobromobimane, 5-chloromethylfluorescein diacetate, carboxy fluorescein diacetate succinimidyl ester, and chloromethyl tetramethylrhodamine are examples of cell

- 15 permeant fluorescent dyes that are used for long term labeling of the cytoplasm of cells.

In a second embodiment, polar tracer molecules such as Lucifer yellow and cascade blue-based fluorescent dyes (Molecular Probes, Inc.) are introduced into cells using bulk loading methods and are also used for cytoplasmic labeling.

- 20 In a third embodiment, antibodies against cytoplasmic components (Sigma Chemical Co.; Molecular Probes, Inc.; Caltag Antibody Co.) are used to fluorescently label the cytoplasm. Examples of cytoplasmic antigens are many of the enzymes involved in intermediary metabolism. Enolase, phosphofructokinase, and acetyl-CoA dehydrogenase are examples of uniformly distributed cytoplasmic antigens.

- 25 In a fourth embodiment, protein chimeras consisting of a cytoplasmic protein genetically fused to an intrinsically luminescent protein such as the green fluorescent protein, or mutants thereof, are used to label the cytoplasm. Fluorescent chimeras of uniformly distributed proteins are used to label the entire cytoplasmic domain. Examples of these proteins are many of the proteins involved in intermediary metabolism and include enolase, lactate dehydrogenase, and hexokinase.

- 30 In a fifth embodiment, antibodies against cytoplasmic antigens (Sigma Chemical Co.; Molecular Probes, Inc.; Caltag Antibody Co.) are used to label cytoplasmic components that are localized in specific cytoplasmic sub-domains.

Examples of these components are the cytoskeletal proteins actin, tubulin, and cytokeratin. A population of these proteins within cells is assembled into discrete structures, which in this case, are fibrous. Fluorescence labeling of these proteins with antibody-based reagents therefore labels a specific sub-domain of the cytoplasm.

5 In a sixth embodiment, non-antibody-based fluorescently labeled molecules that interact strongly with cytoplasmic proteins are used to label specific cytoplasmic components. One example is a fluorescent analog of the enzyme DNase I (Molecular Probes, Inc.) Fluorescent analogs of this enzyme bind tightly and specifically to cytoplasmic actin, thus labeling a sub-domain of the cytoplasm. In another example, 10 fluorescent analogs of the mushroom toxin phalloidin or the drug paclitaxel (Molecular Probes, Inc.) are used to label components of the actin- and microtubule-cytoskeletons, respectively.

In a seventh embodiment, protein chimeras consisting of a cytoplasmic protein genetically fused to an intrinsically luminescent protein such as the green fluorescent 15 protein, or mutants thereof, are used to label specific domains of the cytoplasm. Fluorescent chimeras of highly localized proteins are used to label cytoplasmic sub-domains. Examples of these proteins are many of the proteins involved in regulating the cytoskeleton. They include the structural proteins actin, tubulin, and cytokeratin as well as the regulatory proteins microtubule associated protein 4 and α -actinin.

20

Nuclear labeling

In one embodiment, membrane permeant nucleic-acid-specific luminescent reagents (Molecular Probes, Inc.) are used to label the nucleus of living and fixed cells. These reagents include cyanine-based dyes (e.g., TOTO[®], YOYO[®], and BOBO[™]), 25 phenanthridines and acridines (e.g., ethidium bromide, propidium iodide, and acridine orange), indoles and imidazoles (e.g., Hoechst 33258, Hoechst 33342, and 4',6-diamidino-2-phenylindole), and other similar reagents (e.g., 7-aminoactinomycin D, hydroxystilbamidine, and the psoralens).

In a second embodiment, antibodies against nuclear antigens (Sigma Chemical 30 Co.; Molecular Probes, Inc.; Caltag Antibody Co.) are used to label nuclear components that are localized in specific nuclear domains. Examples of these components are the macromolecules involved in maintaining DNA structure and

function. DNA, RNA, histones, DNA polymerase, RNA polymerase, lamins, and nuclear variants of cytoplasmic proteins such as actin are examples of nuclear antigens.

In a third embodiment, protein chimeras consisting of a nuclear protein genetically fused to an intrinsically luminescent protein such as the green fluorescent protein, or mutants thereof, are used to label the nuclear domain. Examples of these proteins are many of the proteins involved in maintaining DNA structure and function. Histones, DNA polymerase, RNA polymerase, lamins, and nuclear variants of cytoplasmic proteins such as actin are examples of nuclear proteins.

10 **Mitochondrial labeling**

In one embodiment, membrane permeant mitochondrial-specific luminescent reagents (Molecular Probes, Inc.) are used to label the mitochondria of living and fixed cells. These reagents include rhodamine 123, tetramethyl rodamine, JC-1, and the MitoTracker reactive dyes.

15 In a second embodiment, antibodies against mitochondrial antigens (Sigma Chemical Co.; Molecular Probes, Inc.; Caltag Antibody Co.) are used to label mitochondrial components that are localized in specific mitochondrial domains. Examples of these components are the macromolecules involved in maintaining mitochondrial DNA structure and function. DNA, RNA, histones, DNA polymerase, 20 RNA polymerase, and mitochondrial variants of cytoplasmic macromolecules such as mitochondrial tRNA and rRNA are examples mitochondrial antigens. Other examples of mitochondrial antigens are the components of the oxidative phosphorylation system found in the mitochondria (e.g., cytochrome c, cytochrome c oxidase, and succinate dehydrogenase).

25 In a third embodiment, protein chimeras consisting of a mitochondrial protein genetically fused to an intrinsically luminescent protein such as the green fluorescent protein, or mutants thereof, are used to label the mitochondrial domain. Examples of these components are the macromolecules involved in maintaining mitochondrial DNA structure and function. Examples include histones, DNA polymerase, RNA polymerase, and the components of the oxidative phosphorylation system found in the mitochondria (e.g., cytochrome c, cytochrome c oxidase, and succinate dehydrogenase).

Endoplasmic reticulum labeling

In one embodiment, membrane permeant endoplasmic reticulum-specific luminescent reagents (Molecular Probes, Inc.) are used to label the endoplasmic reticulum of living and fixed cells. These reagents include short chain carbocyanine 5 dyes (*e.g.*, DiOC₆ and DiOC₃), long chain carbocyanine dyes (*e.g.*, DiIC₁₆ and DiIC₁₈), and luminescently labeled lectins such as concanavalin A.

In a second embodiment, antibodies against endoplasmic reticulum antigens (Sigma Chemical Co.; Molecular Probes, Inc.; Caltag Antibody Co.) are used to label endoplasmic reticulum components that are localized in specific endoplasmic reticulum 10 domains. Examples of these components are the macromolecules involved in the fatty acid elongation systems, glucose-6-phosphatase, and HMG CoA-reductase.

In a third embodiment, protein chimeras consisting of a endoplasmic reticulum protein genetically fused to an intrinsically luminescent protein such as the green fluorescent protein, or mutants thereof, are used to label the endoplasmic reticulum 15 domain. Examples of these components are the macromolecules involved in the fatty acid elongation systems, glucose-6-phosphatase, and HMG CoA-reductase.

Golgi labeling

In one embodiment, membrane permeant Golgi-specific luminescent reagents (Molecular Probes, Inc.) are used to label the Golgi of living and fixed cells. These 20 reagents include luminescently labeled macromolecules such as wheat germ agglutinin and Brefeldin A as well as luminescently labeled ceramide.

In a second embodiment, antibodies against Golgi antigens (Sigma Chemical Co.; Molecular Probes, Inc.; Caltag Antibody Co.) are used to label Golgi components that are localized in specific Golgi domains. Examples of these components are N- 25 acetylglucosamine phosphotransferase, Golgi-specific phosphodiesterase, and mannose-6-phosphate receptor protein.

In a third embodiment, protein chimeras consisting of a Golgi protein genetically fused to an intrinsically luminescent protein such as the green fluorescent protein, or mutants thereof, are used to label the Golgi domain. Examples of these 30 components are N-acetylglucosamine phosphotransferase, Golgi-specific phosphodiesterase, and mannose-6-phosphate receptor protein.

While many of the examples presented involve the measurement of single cellular processes, this is again intended for purposes of illustration only. Multiple parameter high-content screens can be produced by combining several single parameter screens into a multiparameter high-content screen or by adding cellular parameters to 5 any existing high-content screen. Furthermore, while each example is described as being based on either live or fixed cells, each high-content screen can be designed to be used with both live and fixed cells.

Those skilled in the art will recognize a wide variety of distinct screens that can be developed based on the disclosure provided herein. There is a large and growing list 10 of known biochemical and molecular processes in cells that involve translocations or reorganizations of specific components within cells. The signaling pathway from the cell surface to target sites within the cell involves the translocation of plasma membrane-associated proteins to the cytoplasm. For example, it is known that one of the src family of protein tyrosine kinases, pp60c-src (Walker et al (1993), *J. Biol. Chem.* 268:19552-19558) translocates from the plasma membrane to the cytoplasm 15 upon stimulation of fibroblasts with platelet-derived growth factor (PDGF). Additionally, the targets for screening can themselves be converted into fluorescence-based reagents that report molecular changes including ligand-binding and post-translocational modifications.

20

Example 10. Protease Biosensors

(1) Background

As used herein, the following terms are defined as follows:

- **Reactant** – the parent biosensor that interacts with the proteolytic enzyme.
- 25 • **Product** – the signal-containing proteolytic fragment(s) generated by the interaction of the reactant with the enzyme.
- **Reactant Target Sequence** – an amino acid sequence that imparts a restriction on the cellular distribution of the reactant to a particular subcellular domain of the cell.
- **Product Target Sequence** – an amino acid sequence that imparts a restriction on the 30 cellular distribution of the signal-containing product(s) of the targeted enzymatic reaction to a particular subcellular domain of the cell. If the product is initially localized within a membrane bound compartment, then the Product Target

Sequence must incorporate the ability to export the product out of the membrane-bound compartment. A bi-functional sequence can be used, which first moves the product out of the membrane-bound compartment, and then targets the product to the final compartment. In general, the same amino acid sequences can act as either or both reactant target sequences and product target sequences. Exceptions to this include amino acid sequences which target the nuclear envelope, Golgi apparatus, endoplasmic reticulum, and which are involved in farnesylation, which are more suitable as reactant target sequences.

- 5
- Protease Recognition Site – an amino acid sequence that imparts specificity by mimicking the substrate, providing a specific binding and cleavage site for a protease. Although typically a short sequence of amino acids representing the minimal cleavage site for a protease (e.g. DEVD for caspase-3, Villa, P., S.H. Kaufmann, and W.C. Earnshaw. 1997. Caspases and caspase inhibitors. *Trends Biochem Sci.* 22:388-93), greater specificity may be established by using a longer sequence from an established substrate.
 - 10
 - 15
 - Compartment – any cellular sub-structure or macromolecular component of the cell, whether it is made of protein, lipid, carbohydrate, or nucleic acid. It could be a macromolecular assembly or an organelle (a membrane delimited cellular component). Compartments include, but are not limited to, cytoplasm, nucleus, nucleolus, inner and outer surface of nuclear envelope, cytoskeleton, peroxisome, 20 endosome, lysosome, inner leaflet of plasma membrane, outer leaflet of plasma membrane, outer leaflet of mitochondrial membrane, inner leaflet of mitochondrial membrane, Golgi, endoplasmic reticulum, or extracellular space.
 - 25
 - Signal – an amino acid sequence that can be detected. This includes, but is not limited to inherently fluorescent proteins (e.g. Green Fluorescent Protein), cofactor-requiring fluorescent or luminescent proteins (e.g. phycobiliproteins or luciferases), and epitopes recognizable by specific antibodies or other specific natural or unnatural binding probes, including but not limited to dyes, enzyme cofactors and engineered binding molecules, which are fluorescently or luminescently labeled.
 - 30
 - Also included are site-specifically labeled proteins that contain a luminescent dye. Methodology for site-specific labeling of proteins includes, but is not limited to, engineered dye-reactive amino acids (Post, et al., *J. Biol. Chem.* 269:12880-12887

(1994)), enzyme-based incorporation of luminescent substrates into proteins (Buckler, et al., *Analyt. Biochem.* 209:20-31 (1993); Takashi, *Biochemistry*, 27:938-943 (1988)), and the incorporation of unnatural labeled amino acids into proteins (Noren, et al., *Science*. 244:182-188 (1989)).

- 5 • Detection – a means for recording the presence, position, or amount of the signal. The approach may be direct, if the signal is inherently fluorescent, or indirect, if, for example, the signal is an epitope that must be subsequently detected with a labeled antibody. Modes of detection include, but are not limited to, the spatial position of fluorescence, luminescence, or phosphorescence: (1) intensity; (2) polarization; (3) lifetime; (4) wavelength; (5) energy transfer; and (6) recovery after photobleaching.
- 10

The basic principle of the protease biosensors of the present invention is to spatially separate the reactants from the products generated during a proteolytic reaction. The separation of products from reactants occurs upon proteolytic cleavage of the protease recognition site within the biosensor, allowing the products to bind to, 15 diffuse into, or be imported into compartments of the cell different from those of the reactant. This spatial separation provides a means of quantitating a proteolytic process directly in living or fixed cells. Some designs of the biosensor provide a means of restricting the reactant (uncleaved biosensor) to a particular compartment by a protein sequence ("reactant target sequence") that binds to or imports the biosensor into a 20 compartment of the cell. These compartments include, but are not limited to any cellular substructure, macromolecular cellular component, membrane-limited organelles, or the extracellular space. Given that the characteristics of the proteolytic reaction are related to product concentration divided by the reactant concentration, the spatial separation of products and reactants provides a means of uniquely quantitating 25 products and reactants in single cells, allowing a more direct measure of proteolytic activity.

The molecular-based biosensors may be introduced into cells via transfection and the expressed chimeric proteins analyzed in transient cell populations or stable cell lines. They may also be pre-formed, for example by production in a prokaryotic or 30 eukaryotic expression system, and the purified protein introduced into the cell via a number of physical mechanisms including, but not limited to, micro-injection, scrape loading, electroporation, signal-sequence mediated loading, etc.

Measurement modes may include, but are not limited to, the ratio or difference in fluorescence, luminescence, or phosphorescence: (a) intensity; (b) polarization; or (c) lifetime between reactant and product. These latter modes require appropriate spectroscopic differences between products and reactants. For example, cleaving a reactant containing a limited-mobile signal into a very small translocating component and a relatively large non-translocating component may be detected by polarization. Alternatively, significantly different emission lifetimes between reactants and products allow detection in imaging and non-imaging modes.

One example of a family of enzymes for which this biosensor can be constructed to report activity is the caspases. Caspases are a class of proteins that catalyze proteolytic cleavage of a wide variety of targets during apoptosis. Following initiation of apoptosis, the Class II "downstream" caspases are activated and are the point of no return in the pathway leading to cell death, resulting in cleavage of downstream target proteins. In specific examples, the biosensors described here were engineered to use nuclear translocation of cleaved GFP as a measurable indicator of caspase activation. Additionally, the use of specific recognition sequences that incorporate surrounding amino acids involved in secondary structure formation in naturally occurring proteins may increase the specificity and sensitivity of this class of biosensor.

Another example of a protease class for which this biosensor can be constructed to report activity is zinc metalloproteases. Two specific examples of this class are the biological toxins derived from *Clostridial* species (*C. botulinum* and *C. tetani*) and *Bacillus anthracis*. (Herreros et al. *In The Comprehensive Sourcebook of Bacterial Protein Toxins*. J.E. Alouf and J.H. Freer, Eds. 2nd edition, San Diego, Academic Press, 1999; pp 202-228.) These bacteria express and secrete zinc metalloproteases that enter eukaryotic cells and specifically cleave distinct target proteins. For example, the anthrax protease from *Bacillus anthracis* is delivered into the cytoplasm of target cells via an accessory pore-forming protein, where its proteolytic activity inactivates the MAP-kinase signaling cascade through cleavage of mitogen activated protein kinase kinases 1 or 2 (MEK1 or MEK2). (Leppla, S.A. *In The Comprehensive Sourcebook of Bacterial Protein Toxins*. J.E. Alouf and J.H. Freer, Eds. 2nd edition, San Diego, Academic Press, 1999; pp243-263.) The toxin biosensors described here take

advantage of the natural subcellular localization of these and other target proteins to achieve reactant targeting. Upon cleavage, the signal (with or without a product target sequence) is separated from the reactant to create a high-content biosensor.

One of skill in the art will recognize that the protein biosensors of this aspect of
5 the invention can be adapted to report the activity of any member of the caspase family
of proteases, as well as any other protease, by a substitution of the appropriate protease
recognition site in any of the constructs (see Figure 29B). These biosensors can be
used in high-content screens to detect *in vivo* activation of enzymatic activity and to
identify specific activity based on cleavage of a known recognition motif. This screen
10 can be used for both live cell and fixed end-point assays, and can be combined with
additional measurements to provide a multi-parameter assay.

Thus, in another aspect the present invention provides recombinant nucleic acids
encoding a protease biosensor, comprising:

- a. a first nucleic acid sequence that encodes at least one detectable
15 polypeptide signal;
- b. a second nucleic acid sequence that encodes at least one protease
recognition site, wherein the second nucleic acid sequence is operatively linked to the
first nucleic acid sequence that encodes the at least one detectable polypeptide signal;
and
- c. a third nucleic acid sequence that encodes at least one reactant target
20 sequence, wherein the third nucleic acid sequence is operatively linked to the second
nucleic acid sequence that encodes the at least one protease recognition site.

In this aspect, the first and third nucleic acid sequences are separated by the
25 second nucleic acid sequence, which encodes the protease recognition site.

In a further embodiment, the recombinant nucleic acid encoding a protease
biosensor comprises a fourth nucleic acid sequence that encodes at least one product
target sequence, wherein the fourth nucleic acid sequence is operatively linked to the
first nucleic acid sequence that encodes the at least one detectable polypeptide signal.

30 In a further embodiment, the recombinant nucleic acid encoding a protease
biosensor comprises a fifth nucleic acid sequence that encodes at least one detectable

polypeptide signal, wherein the fifth nucleic acid sequence is operatively linked to the third nucleic acid sequence that encodes the reactant target sequence.

In a preferred embodiment, the detectable polypeptide signal is selected from the group consisting of fluorescent proteins, luminescent proteins, and sequence epitopes. In a most preferred embodiment, the first nucleic acid encoding a polypeptide sequence comprises a sequence selected from the group consisting of SEQ ID NOS: 35, 37, 39, 41, 43, 45, 47, 49, and 51.

In another preferred embodiment, the second nucleic acid encoding a protease recognition site comprises a sequence selected from the group consisting of SEQ ID NOS: 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, and 121. In another preferred embodiment, the third nucleic acid encoding a reactant target sequence comprises a sequence selected from the group consisting of SEQ ID NOS: 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, and 151.

In a most preferred embodiment, the recombinant nucleic acid encoding a protease biosensor comprises a sequence substantially similar to sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, and 33.

In another aspect, the present invention provides a recombinant expression vector comprising nucleic acid control sequences operatively linked to the above-described recombinant nucleic acids. In a still further aspect, the present invention provides genetically engineered host cells that have been transfected with the recombinant expression vectors of the invention.

In another aspect, the present invention provides recombinant protease biosensors comprising

- a. a first domain comprising at least one detectable polypeptide signal;
- b. a second domain comprising at least one protease recognition site; and
- c. a third domain comprising at least one reactant target sequence; wherein the first domain and the third domain are separated by the second domain.

Inherent in this embodiment is the concept that the reactant target sequence restricts the cellular distribution of the reactant, with redistribution of the product occurring after activation (ie: protease cleavage). This redistribution does not require a complete sequestration of products and reactants, as the product distribution can 5 partially overlap the reactant distribution in the absence of a product targeting signal (see below).

In a preferred embodiment, the recombinant protease biosensor further comprises a fourth domain comprising at least one product target sequence, wherein the fourth domain and the first domain are operatively linked and are separated from the 10 third domain by the second domain. In another embodiment, the recombinant protease biosensor further comprises a fifth domain comprising at least one detectable polypeptide signal, wherein the fifth domain and the third domain are operatively linked and are separated from the first domain by the second domain.

In a preferred embodiment, the detectable polypeptide signal domain (first or 15 fifth domain) is selected from the group consisting of fluorescent proteins, luminescent proteins, and sequence epitopes. In a most preferred embodiment, the detectable polypeptide signal domain comprises a sequence selected from the group consisting of SEQ ID NOS:36, 38, 40, 42, 44, 46, 48, 50, and 52.

In another preferred embodiment, the second domain comprising a protease 20 recognition site comprises a sequence selected from the group consisting of SEQ ID NOS:54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, and 122. In another preferred embodiment, the reactant and/or target sequence domains comprise a sequence selected from the group consisting of SEQ ID NOS:124, 126, 128, 130, 132, 25 134, 136, 138, 140, 142, 144, 146, 148, 150, and 152.

In a most preferred embodiment, the recombinant protease biosensor comprises a sequence substantially similar to sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34.

In a still further embodiment, the present invention provides methods and kits 30 for automated analysis of cells, comprising using cells that possess the protease biosensors of the invention to identify compounds that affect protease activity. The

method can be combined with the other methods of the invention in a variety of possible multi-parametric assays.

In these various embodiments, the basic protease biosensor is composed of multiple domains, including at least a first detectable polypeptide signal domain, at 5 least one reactant target domain, and at least one protease recognition domain, wherein the detectable signal domain and the reactant target domain are separated by the protease recognition domain. Thus, the exact order of the domains in the molecule is not generally critical, so long as the protease recognition domain separates the reactant target and first detectable signal domain. For each domain, one or more one of the 10 specified recognition sequences is present.

In some cases, the order of the domains in the biosensor may be critical for appropriate targeting of product(s) and/or reactant to the appropriate cellular compartment(s). For example, the targeting of products or reactants to the peroxisome requires that the peroxisomal targeting domain comprise the last three amino acids of 15 the protein. Determination of those biosensor in which the relative placement of targeting domains within the biosensor is critical can be determined by one of skill in the art through routine experimentation.

Some examples of the basic organization of domains within the protease biosensor are shown in Figure 30. One of skill in the art will recognize that any one of 20 a wide variety of protease recognition sites, product target sequences, polypeptide signals, and/or product target sequences can be used in various combinations in the protein biosensor of the present invention, by substituting the appropriate coding sequences into the multi-domain construct. Non-limiting examples of such alternative sequences are shown in Figure 29A-29C. Similarly, one of skill in the art will 25 recognize that modifications, substitutions, and deletions can be made to the coding sequences and the amino acid sequence of each individual domain within the biosensor, while retaining the function of the domain. Such various combinations of domains and modifications, substitutions and deletions to individual domains are within the scope of the invention.

As used herein, the term "coding sequence" or a sequence which "encodes" a 30 particular polypeptide sequence, refers to a nucleic acid sequence which is transcribed (in the case of DNA) and translated (in the case of mRNA) into a polypeptide in vitro

or in vivo when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but is not limited to, cDNA from prokaryotic or eukaryotic mRNA, 5 genomic DNA sequences from prokaryotic or eukaryotic DNA, and synthetic DNA sequences. A transcription termination sequence will usually be located 3' to the coding sequence.

As used herein, the term DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription 10 termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the transcription and translation of a coding sequence in a host cell. Not all of these control sequences need always be present in a recombinant vector so long as the DNA sequence of interest is capable of being transcribed and translated appropriately.

15 As used herein, the term "operatively linked" refers to an arrangement of elements wherein the components so described are configured so as to perform their usual function. Thus, control sequences operatively linked to a coding sequence are capable of effecting the expression of the coding sequence. The control sequences need not be contiguous with the coding sequence, so long as they function to direct the 20 expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between a promoter sequence and the coding sequence and the promoter sequence can still be considered "operatively linked" to the coding sequence.

Furthermore, a nucleic acid coding sequence is operatively linked to another 25 nucleic acid coding sequences when the coding region for both nucleic acid molecules are capable of expression in the same reading frame. The nucleic acid sequences need not be contiguous, so long as they are capable of expression in the same reading frame. Thus, for example, intervening coding regions can be present between the specified nucleic acid coding sequences, and the specified nucleic acid coding regions can still be 30 considered "operatively linked".

The intervening coding sequences between the various domains of the biosensors can be of any length so long as the function of each domain is retained.

Generally, this requires that the two-dimensional and three-dimensional structure of the intervening protein sequence does not preclude the binding or interaction requirements of the domains of the biosensor, such as product or reactant targeting, binding of the protease of interest to the biosensor, fluorescence or luminescence of the detectable 5 polypeptide signal, or binding of fluorescently labeled epitope-specific antibodies.

One case where the distance between domains of the protease biosensor is important is where the goal is to create a fluorescence resonance energy transfer pair. In this case, the FRET signal will only exist if the distance between the donor and acceptor is sufficiently small as to allow energy transfer (Tsien, Heim and Cubbit, WO 10 97/28261). The average distance between the donor and acceptor moieties should be between 1 nm and 10 nm with a preference of between 1 nm and 6 nm. This is the physical distance between donor and acceptor. The intervening sequence length can vary considerably since the three dimensional structure of the peptide will determine the physical distance between donor and acceptor.

15 "Recombinant expression vector" includes vectors that operatively link a nucleic acid coding region or gene to any promoter capable of effecting expression of the gene product. The promoter sequence used to drive expression of the protease biosensor may be constitutive (driven by any of a variety of promoters, including but not limited to, CMV, SV40, RSV, actin, EF) or inducible (driven by any of a number of 20 inducible promoters including, but not limited to, tetracycline, ecdysone, steroid-responsive). The expression vector must be replicable in the host organisms either as an episome or by integration into host chromosomal DNA. In a preferred embodiment, the expression vector comprises a plasmid. However, the invention is intended to include any other suitable expression vectors, such as viral vectors.

25 The phrase "substantially similar" is used herein in reference to the nucleotide sequence of DNA, or the amino acid sequence of protein, having one or more conservative or non-conservative variations from the protease biosensor sequences disclosed herein, including but not limited to deletions, additions, or substitutions wherein the resulting nucleic acid and/or amino acid sequence is functionally 30 equivalent to the sequences disclosed and claimed herein. Functionally equivalent sequences will function in substantially the same manner to produce substantially the same protease biosensor as the nucleic acid and amino acid compositions disclosed and

claimed herein. For example, functionally equivalent DNAs encode protease biosensors that are the same as those disclosed herein or that have one or more conservative amino acid variations, such as substitutions of non-polar residues for other non-polar residues or charged residues for similarly charged residues, or addition 5 to/deletion from regions of the protease biosensor not critical for functionality. These changes include those recognized by those of skill in the art as substitutions, deletions, and/or additions that do not substantially alter the tertiary structure of the protein.

As used herein, substantially similar sequences of nucleotides or amino acids share at least about 70%-75% identity, more preferably 80-85% identity, and most 10 preferably 90-95% identity. It is recognized, however, that proteins (and DNA or mRNA encoding such proteins) containing less than the above-described level of homology (due to the degeneracy of the genetic code) or that are modified by conservative amino acid substitutions (or substitution of degenerate codons) are contemplated to be within the scope of the present invention.

15 The term "heterologous" as it relates to nucleic acid sequences such as coding sequences and control sequences, denotes sequences that are not normally associated with a region of a recombinant construct, and/or are not normally associated with a particular cell. Thus, a "heterologous" region of a nucleic acid construct is an identifiable segment of nucleic acid within or attached to another nucleic acid molecule 20 that is not found in association with the other molecule in nature. For example, a heterologous region of a construct could include a coding sequence flanked by sequences not found in association with the coding sequence in nature. Another example of a heterologous coding sequence is a construct where the coding sequence itself is not found in nature (e.g., synthetic sequences having codons different from the 25 native gene). Similarly, a host cell transformed with a construct which is not normally present in the host cell would be considered heterologous for purposes of this invention.

Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), 30 *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in *Methods in Enzymology* (M.P. Deutshcer, ed., (1990) Academic Press, Inc.); *PCR*

Protocols: A Guide to Methods and Applications (Innis, et al. 1990. Academic Press, San Diego, CA), Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed. (R.I. Freshney. 1987. Liss, Inc. New York, NY), Gene Transfer and Expression Protocols, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 5 1998 Catalog (Ambion, Austin, TX).

The biosensors of the present invention are constructed and used to transfect host cells using standard techniques in the molecular biological arts. Any number of such techniques, all of which are within the scope of this invention, can be used to generate protease biosensor-encoding DNA constructs and genetically transfected host 10 cells expressing the biosensors. The non-limiting examples that follow demonstrate one such technique for constructing the biosensors of the invention.

EXAMPLE OF PROTEASE BIOSENSOR CONSTRUCTION AND USE:

In the following examples, caspase-specific biosensors with specific product 15 target sequences have been constructed using sets of 4 primers (2 sense and 2 antisense). These primers have overlap regions at their termini, and are used for PCR via a primer walking technique. (Sambrook, J., Fritsch, E.F. and Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York) The two sense primers were chosen to start from the 5' 20 polylinker (BspI) of the GFP-containing vector (Clontech, California) to the middle of the designed biosensor sequence. The two antisense primers start from a 3' GFP vector site (Bam HI), and overlap with the sense primers by 12 nucleotides in the middle.

PCR conditions were as follows: 94°C for 30 seconds for denaturation, 55°C for 25 30 seconds for annealing, and 72°C for 30 seconds for extension for 15 cycles. The primers have restriction endonuclease sites at both ends, facilitating subsequent cloning of the resulting PCR product.

The resulting PCR product was gel purified, cleaved at BspE1 and BamH1 restriction sites present in the primers, and the resulting fragment was gel purified. Similarly, the GFP vector (Clontech, San Francisco, CA) was digested at BspE1 and 30 BamH1 sites in the polylinker. Ligation of the GFP vector and the PCR product was performed using standard techniques at 16°C overnight. *E. coli* cells were transfected

with the ligation mixtures using standard techniques. Transformed cells were selected on LB-agar with an appropriate antibiotic.

Cells and transfections. For DNA transfection, BHK cells and MCF-7 cells
5 were cultured to 50-70% confluence in 6 well plates containing 3 ml of minimal
Eagle's medium (MEM) with 10% fetal calf serum, 1 mM L-glutamine, 50 µg/ml
streptomycin, 50 µg/ml penicillin, 0.1 mM non-essential amino acids, 1 mM sodium
pyruvate and 10 µg/ml of bovine insulin (for MCF-7 cell only) at 37 °C in a 5% CO₂
incubator for about 36 hours. The cells were washed with serum free MEM media and
10 incubated for 5 hours with 1 ml of transfection mixture containing 1 µg of the
appropriate plasmid and 4 µg of lipofectimine (BRL) in the serum free MEM media.
Subsequently, the transfection medium was removed and replaced with 3 ml of normal
culture media. The transfected cells were maintained in growth medium for at least 16
hours before performing selection of the stable cells based on standard molecular
15 biology methods (Ausubel, et al 1995).

Apoptosis assay. For apoptosis assays, the cells (BHK, MCF-7) stably
transfected with the appropriate protease biosensor expression vector were plated on
tissue culture treated 96-well plates at 50-60% confluence and cultured overnight at
20 37°C, 5% CO₂. Varying concentrations of cis-platin, staurosporine, or paclitaxel in
normal culture media were freshly prepared from stock and added to cell culture dishes
to replace the old culture media. The cells were then observed with the cell screening
system of the present invention at the indicated time points either as live cell
experiments or as fixed end-point experiments.

25

1. Construction of 3-domain protease biosensors
 - a. Caspase-3 biosensor with an annexin II reactant targeting domain (pljkGFP).

The design of this biosensor is outlined in Figure 31, and its sequence is shown
30 in SEQ ID NO:1 and 2.

Primers for Caspase 3, Product target sequence = none (CP3GFP-CYTO):

- 1) TCA TCA TCC GGA GCT GGA GCC GGA GCT GGC CGA TCG GCT GTT
AAA TCT GAA GGA AAG AGA AAG TGT GAC GAA GTT GAT GGA ATT
5 GAT GAA GTA GCA (SEQ ID NO:153)
- 2) GAA GAA GGA TCC GGC ACT TGG GGG TGT AGA ATG AAC ACC
CTC CAA GCT GAG CTT GCA CAG GAT TTC GTG GAC AGT AGA
CAT AGT ACT TGC TAC TTC ATC (SEQ ID NO:154)
- 3) TCA TCA TCC GGA GCT GGA (SEQ ID NO:155)
- 10 4) GAA GAA GGA TCC GGC ACT (SEQ ID NO:156)

This biosensor is restricted to the cytoplasm by the reactant target sequence. The reactant target sequence is the annexin II cytoskeletal binding domain (MSTVHEILCKLSLEGVHSTPPSA) (SEQ ID NO:124) (Figure 29C) (Eberhard et al. 1997. *Mol. Biol. Cell* 8:293a). The enzyme recognition site corresponds to two copies of the amino acid sequence DEVD (SEQ ID NO:60) (Figure 29B), which serves as the recognition site of caspase-3. Other examples with different numbers of protease recognition sites and/or additional amino acids from a naturally occurring protease recognition site are shown below. The signal domain is EGFP (SEQ ID NO:46) (Figure 29A) (Clontech, California). The parent biosensor (the reactant) is restricted to the cytoplasm by binding of the annexin II domain to the cytoskeleton, and is therefore excluded from the nucleus. Upon cleavage of the protease recognition site by caspase 3, the signal domain (EGFP) is released from the reactant targeting domain (annexin II), and is distributed throughout the whole volume of the cell, because it lacks any specific targeting sequence and is small enough to enter the nucleus passively. (Fig 32)

The biosensor response is measured by quantitating the effective cytoplasm-to-nuclear translocation of the signal (see above). Measurement of the response is by one of several modes, including integrated or average nuclear region intensity, the ratio or difference of the integrated or average cytoplasm intensity to integrated or average nuclear intensity. The nucleus is defined using a DNA-specific dye, such as Hoechst 33342.

This biosensor provides a measure of the proteolytic activity around the annexin II cytoskeleton binding sites within the cell. Given the dispersed nature of the cytoskeleton and the effectively diffuse state of cytosolic enzymes, this provides an effective measure of the cytoplasm in general.

5

Results & Discussion:

Fig 32 illustrates images before and after stimulation of apoptosis by cis-platin in BHK cells, transfected with the caspase 3 biosensor. The images clearly illustrate accumulation of fluorescence in the nucleus. Generation of the spatial change in 10 fluorescence is non-reversible and thus the timing of the assay is flexible. Controls for this biosensor include using a version in which the caspase-3-specific site has been omitted. In addition, disruption of the cytoskeleton with subsequent cell rounding did not produce the change in fluorescence distribution. Our experiments demonstrate the correlation of nuclear condensation with activation of caspase activity. We have also 15 tested this biosensor in MCF-7 cells. A recent report measured a peak response in caspase-3 activity 6 h after stimulation of MCF-7 cells with etoposide accompanied by cleavage of PARP (Benjamin et al. 1998. *Mol Pharmacol.* 53:446-50). However, another recent report found that MCF-7 cells do not possess caspase-3 activity and, in fact, the caspase-3 gene is functionally deleted (Janicke et al. 1998. *J Biol Chem.* 20 273:9357-60). Caspase-3 activity was not detected with the caspase biosensor in MCF-7 cells after a 15 h treatment with 100 µM etoposide.

Janicke et al., (1998) also indicated that many of the conventional substrates of caspase-3 were cleaved in MCF-7 cells upon treatment with staurosporine. Our experiments demonstrate that caspase activity can be measured using the biosensor in 25 MCF-7 cells when treated with staurosporine. The maximum magnitude of the activation by staurosporine was approximately one-half that demonstrated with cis-platin in BHK cells. This also implies that the current biosensor, although designed to be caspase-3-specific, is indeed specific for a class of caspases rather than uniquely specific for caspase-3. The most likely candidate is caspase-7 (Janicke et al., 1998). 30 These experiments also demonstrated that the biosensor can be used in multiparameter experiments, with the correlation of decreases in mitochondrial membrane potential, nuclear condensation, and caspase activation.

We have specifically tested the effects of paclitaxel on caspase activation using the biosensor. Caspase activity in BHK and MCF-7 cells was stimulated by paclitaxel. It also appears that caspase activation occurred after nuclear morphology changes. One caveat is that, based on the above discussions, the caspase activity reported by the 5 biosensor in this assay is likely to be due to the combination of caspase-3 and, at least, caspase-7 activity.

Consistent with the above results using staurosporine stimulation on MCF-7 cells, paclitaxel also stimulated the activation of caspase activity. The magnitude was similar to that of staurosporine. This experiment used a much narrower range of 10 paclitaxel than previous experiments where nuclear condensation appears to dominate the response.

b. Caspase biosensor with the microtubule associated protein 4 (MAP4) projection domain (CP8GFPNLS-SIZEPROJ)

15 Another approach for restricting the reactant to the cytoplasm is to make the biosensor too large to penetrate the nuclear pores. Cleavage of such a biosensor liberates a product capable of diffusing into the nucleus.

The additional size required for this biosensor is provided by using the projection domain of MAP4 (SEQ ID NO:142) (Figure 29C) (CP8GFPNLS- 20 SIZEPROJ). The projection domain of MAP4 does not interact with microtubules on its own, and, when expressed, is diffusely distributed throughout the cytoplasm, but is excluded from the nucleus due to its size (~120 kD). Thus, this biosensor is distinct from the one using the full length MAP4 sequence. (see below) One of skill in the art will recognize that many other such domains could be substituted for the MAP4 25 projection domain, including but not limited to multiple copies of any GFP or one or more copies of any other protein that lacks an active NLS and exceeds the maximum size for diffusion into the nucleus (approximately 60 kD; Alberts, B., Bray, D., Raff, M., Roberts, K., Watson, J.D. (Eds.) Molecular Biology of the Cell, third edition, New York: Garland publishing, 1994. pp 561-563). The complete sequence of the resulting 30 biosensor is shown in SEQ ID NO: 3-4. A similar biosensor with a different protease recognition domain is shown in SEQ ID NO:5-6.

c. Caspase biosensor with a nuclear export signal

Another approach for restricting the reactant to the cytoplasm is to actively restrict the reactant from the nucleus by using a nuclear export signal. Cleavage of such a biosensor liberates a product capable of diffusing into the nucleus.

5 The *Bacillus anthracis* bacterium expresses a zinc metalloprotease protein complex called anthrax protease. Human mitogen activated protein kinase kinase 1 (MEK 1) (Seger et al., J. Biol. Chem. 267:25628-25631, 1992) possesses an anthrax protease recognition site (amino acids 1-13) (SEQ ID NO:102) (Figure 29B) that is cleaved after amino acid 8, as well as a nuclear export signal at amino acids 32-44
10 (SEQ ID NO:140) (Figure 29C). Human MEK 2 (Zheng and Guan, J. Biol. Chem. 268:11435-11439, 1993) possesses an anthrax protease recognition site comprising amino acid residues 1-16 (SEQ ID NO:104) (Figure 29B) and a nuclear export signal at amino acids 36-48. (SEQ ID NO:148) (Figure 29C).

15 The anthrax protease biosensor comprises Fret25 (SEQ ID NO:48) (Figure 29A) as the signal, the anthrax protease recognition site, and the nuclear export signal from MEK 1 or MEK2. (SEQ ID NOS: 7-8 (MEK1); 9-10 (MEK2)) The intact biosensor will be retained in the cytoplasm by virtue of this nuclear export signal (eg., the reactant target site). Upon cleavage of the fusion protein by anthrax protease, the NES will be separated from the GFP allowing the GFP to diffuse into the nucleus.
20

2. Construction of 4- and 5-domain biosensors

For all of the examples presented above for 3-domain protease biosensors, a product targeting sequence, including but not limited to those in Figure 29C, such as a nuclear localization sequence (NLS), can be operatively linked to the signal sequence,
25 and thus cause the signal sequence to segregate from the reactant target domain after proteolytic cleavage. Addition of a second detectable signal domain, including but not limited to those in Figure 29A, operatively linked with the reactant target domain is also useful in allowing measurement of the reaction by multiple means. Specific examples of such biosensors are presented below.
30

a. 4 domain biosensors

1. Caspase biosensors with nuclear localization sequences

(pcas3nlsGFP; CP3GFPNLS-CYTO):

The design of the biosensor is outlined in **Figure 33**, and its sequence is shown in **SEQ ID NO:11-12**. PCR and cloning procedures were performed as described above, except that the following oligonucleotides were used:

5 Primers for Caspase 3, Product target sequence = NLS (CP3GFPNLS-CYTO) :

- 1) TCA TCA TCC GGA AGA AGG AAA CGA CAA AAG CGA TCG GCT
GTT AAA TCT GAA GGA AAG AGA AAG TGT GAC GAA GTT GAT GGA
ATT GAT GAA GTA GCA (**SEQ ID NO:157**)
- 10 2) GAA GAA GGA TCC GGC ACT TGG GGG TGT AGA ATG AAC ACC
CTC CAA GCT GAG CTT GCA CAG GAT TTC GTG GAC AGT AGA
CAT AGT ACT TGC TAC TTC ATC (**SEQ ID NO:154**)
- 3) TCA TCA TCC GGA AGA AGG (**SEQ ID NO:158**)
- 4) GAA GAA GGA TCC GGC ACT (**SEQ ID NO:156**)

15

- This biosensor is similar to that shown in **SEQ ID NO:2** except upon recognition and cleavage of the protease recognition site, the product is released and the signal accumulates specifically in the nucleus due to the presence of a nuclear localization sequence, RRKRQK (**SEQ ID NO:128**) (**Figure 29C**)(Briggs et al., J. Biol. Chem. 273:22745, 1998) attached to the signal. A specific benefit of this construct is that the products are clearly separated from the reactants. The reactants remain in the cytoplasm, while the product of the enzymatic reaction is restricted to the nuclear compartment. The response is measured by quantitating the effective cytoplasm-to-nuclear translocation of the signal, as described above.
- 25 With the presence of both product and reactant targeting sequences in the parent biosensor, the reactant target sequence should be dominant prior to activation (e.g., protease cleavage) of the biosensor. One way to accomplish this is by masking the product targeting sequence in the parent biosensor until after protease cleavage. In one such example, the product target sequence is functional only when relatively near the
- 30 end of a polypeptide chain (ie: after protease cleavage). Alternatively, the biosensor may be designed so that its tertiary structure masks the function of the target sequence until after protease cleavage. Both of these approaches include comparing targeting

sequences with different relative strengths for targeting. Using the example of the nuclear localization sequence (NLS) and annexin II sequences, different strengths of NLS have been tried with clone selection based on cytoplasmic restriction of the parent biosensor. Upon activation, the product targeting sequence will naturally dominate the 5 localization of its associated detectable sequence domain because it is then separated from the reactant targeting sequence.

An added benefit of using this biosensor is that the product is targeted, and thus concentrated, into a smaller region of the cell. Thus, smaller amounts of product are detectable due to the increased concentration of the product. This concentration effect 10 is relatively insensitive to the cellular concentration of the reactant. The signal-to-noise ratio (SNR) of such a measurement is improved over the more dispersed distribution of biosensor #1.

Similar biosensors that incorporate either the caspase 6 (SEQ ID NO:66) (Figure 29B) or the caspase 8 protease recognition sequence (SEQ ID NO:74) (Figure 15 29B) can be made using the methods described above, but using the following primer sets:

Primers for Caspase 6, Product target sequence = NLS (CP6GFPNLS-CYTO)

- 1) TCA TCA TCC GGA AGA AGG AAA CGA CAA AAG CGA TCG
20 ACA AGA CTT GTT GAA ATT GAC AAC (SEQ ID NO:159)
- 2) GAA GAA GGA TCC GGC ACT TGG GGG TGT AGA ATG AAC
ACC CTC CAA GCT GAG CTT GCA CAG GAT TTC GTG GAC
AGT AGA CAT AGT ACT GTT GTC AAT TTC (SEQ ID NO:160)

- 25 3) TCA TCA TCC GGA AGA AGG (SEQ ID NO:158)
- 4) GAA GAA GGA TCC GGC ACT (SEQ ID NO:156)

Primers for Caspase 8, Product target sequence = NLS (CP8GFPNLS-CYTO)

- 1) TCA TCA TCC GGA AGA AGG AAA CGA CAA AAG CGA TCG
30 TAT CAA AAA GGA ATA CCA GTT GAA ACA GAC AGC GAA GAG
CAA CCT TAT (SEQ ID NO:161)
- 2) GAA GAA GGA TCC GGC ACT TGG GGG TGT AGA ATG AAC ACC CTC

CAA GCT GAG CTT GCA CAG GAT TTC GTG GAC AGT AGA CAT AGT
ACT ATA AGG TTG CTC (SEQ ID NO:162)

- 3) TCA TCA TCC GGA AGA AGG (SEQ ID NO:158)
- 4) GAA GAA GGA TCC GGC ACT (SEQ ID NO:156)

5

The sequence of the resulting biosensors is shown in SEQ ID NO:13-14 (Caspase 6) and SEQ ID NO: 15-16 (Caspase 8). Furthermore, multiple copies of the protease recognition sites can be inserted into the biosensor, yielding the biosensors shown in SEQ ID NO: 17-18 (Caspase 3) and SEQ ID NO:19-20 (Caspase 8).

10

2. Caspase 3 biosensor with a second signal domain

An alternative embodiment employs a second signal domain operatively linked to the reactant target domain. In this example, full length MAP4 serves as the reactant target sequence. Upon recognition and cleavage, one product of the reaction, containing the reactant target sequence, remains bound to microtubules in the cytoplasm with its own unique signal, while the other product, containing the product target sequence, diffuses into the nucleus. This biosensor provides a means to measure two activities at once: caspase 3 activity using a translocation of GFP into the nucleus and microtubule cytoskeleton integrity in response to signaling cascades initiated during apoptosis, monitored by the MAP4 reactant target sequence.

The basic premise for this biosensor is that the reactant is tethered to the microtubule cytoskeleton by virtue of the reactant target sequence comprising the full length microtubule associated protein MAP4 (SEQ ID NO:152) (Figure 29C). In this case, a DEVD (SEQ ID NO:60) (Figure 29B) recognition motif is located between the EYFP signal (SEQ ID NO:44) (Figure 29A) operatively linked to the reactant target sequence, as well as the EBFP signal (SEQ ID NO:48) (Figure 29A) operatively linked to the C-terminus of MAP4. The resulting biosensor is shown in SEQ ID NO:21-22.

This biosensor can also include a product targeting domain, such as an NLS, 30 operatively linked to the signal domain.

With this biosensor, caspase-3 cleavage still releases the N-terminal GFP, which undergoes translocation to the nucleus (directed there by the NLS). Also, the MAP4

fragment, which is still intact following proteolysis by caspase-3, continues to report on the integrity of the microtubule cytoskeleton during the process of apoptosis via the second GFP molecule fused to the C-terminus of the biosensor. Therefore, this single chimeric protein allows simultaneous analysis of caspase-3 activity and the 5 polymerization state of the microtubule cytoskeleton during apoptosis induced by a variety of agents. This biosensor is also useful for analysis of potential drug candidates that specifically target the microtubule cytoskeleton, since one can determine whether a particular drug induced apoptosis in addition to affecting microtubules.

This biosensor potentially combines a unique signal for the reactant, 10 fluorescence resonance energy transfer (FRET) from signal 2 to signal 1, and a unique signal localization for the product, nuclear accumulation of signal 1. The amount of product generated will also be indicated by the magnitude of the loss in FRET, but this will be a smaller SNR than the combination of FRET detection of reactant and spatial localization of the product.

15 FRET can occur when the emission spectrum of a donor overlaps significantly the absorption spectrum of an acceptor molecule. (dos Remedios, C.G., and P.D. Moens. 1995. Fluorescence resonance energy transfer spectroscopy is a reliable "ruler" for measuring structural changes in proteins. Dispelling the problem of the unknown orientation factor. *J Struct Biol.* 115:175-85; Emmanouilidou, E., A.G. Teschemacher, 20 A.E. Pouli, L.I. Nicholls, E.P. Seward, and G.A. Rutter. 1999. Imaging Ca(2+) concentration changes at the secretory vesicle surface with a recombinant targeted cameleon. *Curr Biol.* 9:915-918.) The average physical distance between the donor and acceptor molecules should be between 1 nm and 10 nm with a preference of between 1 nm and 6 nm. The intervening sequence length can vary considerably since the three 25 dimensional structure of the peptide will determine the physical distance between donor and acceptor. This FRET signal can be measured as (1) the amount of quenching of the donor in the presence of the acceptor, (2) the amount of acceptor emission when exciting the donor, and/or (3) the ratio between the donor and acceptor emission. Alternatively, fluorescent lifetimes of donor and acceptor could be measured.

30 This case adds value to the above FRET biosensor by nature of the existence of the reactant targeting sequence. This sequence allows the placement of the biosensor

into specific compartments of the cell for a more direct readout of activity in those compartments such as the inner surface of the plasma membrane.

The cytoplasmic second signal represents both original reactant plus one part of the product. The nuclear first signal represents another product of the reaction. Thus the 5 enzymatic reaction has the added flexibility in that it can be represented as (1) nuclear intensity; (2) the nucleus /cytoplasm ratio; (3) the nucleus /cytoplasm FRET ratio; (4) cytoplasmic /cytoplasmic FRET ratio.

The present FRET biosensor design differs from previous FRET-based biosensors (see WO 97/28261; WO9837226) in that it signal measurement is based on 10 spatial position rather than intensity. The products of the reaction are segregated from the reactants. It is this change in spatial position that is measured. The FRET-based biosensor is based on the separation, but not to another compartment, of a donor and acceptor pair. The intensity change is due to the physical separation of the donor and acceptor upon proteolytic cleavage. The disadvantages of FRET-based biosensors are 15 (1) the SNR is rather low and difficult to measure, (2) the signal is not fixable. It must be recorded using living cells. Chemical fixation, for example with formaldehyde, cannot preserve both the parent and resultant signal; (3) the range of wavelengths are limiting and cover a larger range of the spectrum due to the presence of two fluorophores or a fluorophore and chromophore; (4) the construction has greater 20 limitations in that the donor and acceptor must be precisely arranged to ensure that the distance falls within 1-10 nm.

Benefits of the positional biosensor includes: (1) ability to concentrate the signal in order to achieve a higher SNR. (2) ability to be used with either living or fixed cells; (3) only a single fluorescent signal is needed; (4) the arrangement of the domains 25 of the biosensor is more flexible. The only limiting factor in the application of the positional biosensor is the need to define the spatial position of the signal which requires an imaging method with sufficient spatial resolution to resolve the difference between the reactant compartment and the product compartment.

One of skill in the art will recognize that this approach can be adapted to report 30 any desired combination of activities by simply making the appropriate substitutions for the protease recognition sequence and the reactant target sequence, including but not limited to those sequences shown in Figure 29A-C.

3. Caspase 8 biosensor with a nucleolar localization domain (CP8GFPNUC-CYTO)

This approach (diagrammed in Figure 34) utilizes a biosensor for the detection
5 of caspase-8 activity. In this biosensor, a nucleolar localization signal
(RKIRITYLKSCRRMKRSGFEMSRPIPSHLT) (SEQ ID NO:130) (Figure 29C)
(Ueki et al., Biochem. Biophys. Res. Comm. 252:97-100, 1998) was used as the
product target sequence, and made by PCR using the primers described below. The
10 PCR product was digested with BspE1 and PvuI and gel purified. The vector and the
PCR product were ligated as described above.

Primers for Caspase 8, Nucleolar localization signal (CP8GFPNUC-CYTO):

- 1) TCA TCA TCC GGA AGA AAA CGT ATA CGT ACT TAC CTC AAG
15 TCC TGC AGG CGG ATG AAA AGA (SEQ ID NO:163)
- 2) GAA GAA CGA TCG AGT AAG GTG GGA AGG AAT AGG TCG AGA
CAT CTC AAA ACC ACT TCT TTT CAT (SEQ ID NO:164)
- 3) TCA TCA TCC GGA AGA AAA (SEQ ID NO:165)
- 4) GAA GAA CGA TCG AGT AAG (SEQ ID NO:166)

20 The sequence of the resulting biosensor is shown in SEQ ID NO: 23-24. This
biosensor includes the protease recognition site for caspase-8 (SEQ ID NO:74)
(Figure 29B). A similar biosensor utilizes the protease recognition site for caspase-3.
(SEQ ID NO:25-26)

25 These biosensors could be used with other biosensors that possess the same
product signal color that are targeted to separate compartments, such as CP3GFPNLS-
CYTO. The products of each biosensor reaction can be uniquely measured due to
separation of the products based on the product targeting sequences. Both products
from CP8GFPNUC-CYTO and CP3GFPNLS-CYTO are separable due to the different
30 spatial positions, nucleus vs. nucleolus, even though the colors of the products are
exactly the same. Assessing the non-nucleolar, nuclear region in order to avoid the
spatial overlap of the two signals would perform the measurement of CP3GFPNLS in

the presence of CP8GFPNUC. The loss of the nucleolar region from the nuclear signal is insignificant and does not significantly affect the SNR. The principle of assessing multiple parameters using the same product color significantly expands the number of parameters that can be assessed simultaneously in living cells. This concept can be
5 extended to other non-overlapping product target compartments.

Measurement of translocation to the nucleolar compartment is performed by (1) defining a mask corresponding to the nucleolus based on a nucleolus-specific marker, including but not limited to an antibody to nucleolin (Lischwe et al., 1981. *Exp. Cell Res.* 136:101-109); (2) defining a mask for the reactant target compartment, and (3)
10 determining the relative distribution of the signal between these two compartments. This relative distribution could be represented by the difference in the two intensities or, preferably, the ratio of the intensities between compartments.

The combination of multiple positional biosensors can be complicated if the reactant compartments are overlapping. Although each signal could be measured by
15 simply determining the amount of signal in each product target compartment, higher SNR will be possible if each reactant is uniquely identified and quantitated. This higher SNR can be maximized by adding a second signal domain of contrasting fluorescent property. This second signal may be produced by a signal domain operatively linked to the product targeting sequence, or by FRET (see above), or by a reactant targeting
20 sequence uniquely identifying it within the reactant compartment based on color, spatial position, or fluorescent property including but not limited to polarization or lifetime. Alternatively, for large compartments, such as the cytoplasm, it is possible to place different, same colored biosensors in different parts of the same compartment.

25 **4. Protease biosensors with multiple copies of a second signal domain serving as a reactant target domain**

In another example, (CP8YFPNLS-SIZECFPn) increasing the size of the reactant is accomplished by using multiple inserts of a second signal sequence, for example, ECFP (SEQ ID NO:50) (Figure 29A) (Tsien, R.Y. 1998. *Annu Rev Biochem.* 67:509-44). Thus, the multiple copies of the second signal sequence serve as the reactant target domain by excluding the ability of the biosensor to diffuse into the nucleus. This type of biosensor provides the added benefit of additional signal being

available per biosensor molecule. Aggregation of multiple fluorescent probes also can result in unique signals being manifested, such as FRET, self quenching, eximer formation, etc. This could provide a unique signal to the reactants.

5 **5. Tetanus/botulinum biosensor with trans-membrane targeting domain**

In an alternative embodiment, a trans-membrane targeting sequence is used to tether the reactant to cytoplasmic vesicles, and an alternative protease recognition site is used. The tetanus/botulinum biosensor (SEQ ID NOS:27-28 (cellubrevin); 29-30 (synaptobrevin) consists of an NLS (SEQ ID NO:128) (Figure 29C), Fret25 signal domain (SEQ ID NO:52) (Figure 29A), a tetanus or botulinum zinc metalloprotease recognition site from cellubrevin (SEQ ID NO:106) (Figure 29B) (McMahon et al., Nature 364:346-349, 1993; Martin et al., J. Cell Biol., in press) or synaptobrevin (SEQ ID NO:108) (Figure 29B) (GenBank Accession #U64520), and a trans-membrane sequence from cellubrevin (SEQ ID NO:146) (Figure 29C) or synaptobrevin (SEQ ID NO:144) (Figure 29C) at the 3'-end which tethers the biosensor to cellular vesicles. The N-terminus of each protein is oriented towards the cytoplasm. In the intact biosensor, GFP is tethered to the vesicles. Upon cleavage by the tetanus or botulinum zinc metalloprotease, GFP will no longer be associated with the vesicle and is free to diffuse throughout the cytoplasm and the nucleus.

b. **5-domain biosensors**

1. **Caspase 3 biosensor with a nuclear localization domain and a second signal domain operatively linked to an annexin II domain**

25 The design of this biosensor is outlined in Figure 35, and the sequence is shown in SEQ ID NO:33-34. This biosensor differs from SEQ ID NO 11-12 by including a second detectable signal, ECFP (SEQ ID NO:50) (Figure 29A) (signal 2) operatively linked to the reactant target sequence.

30 **2. Caspase 3 biosensor with a nuclear localization sequence and a second signal domain operatively linked to a MAP4 projection domain (CP3YFPNLS-CFPCYTO)**

In this biosensor (SEQ ID NO:31-32), an NLS product targeting domain (SEQ ID NO:128) (Figure 29C) is present upstream of an EYFP signal domain (SEQ ID NO:44) (Figure 29A). A DEVD protease recognition domain (SEQ ID NO:60) (Figure 29B) is between after the EYFP signal domain and before the MAP4 projection domain (SEQ ID NO:142) (Figure 29C).

Example 11. Fluorescent Biosensor Toxin Characterization

As used herein, "toxin" refers to any organism, macromolecule, or organic or inorganic molecule or ion that alters normal physiological processes found within a cell, or any organism, macromolecule, or organic or inorganic molecule or ion that alters the physiological response to modulators of known physiological processes. Thus, a toxin can mimic a normal cell stimulus, or can alter a response to a normal cell stimulus.

Living cells are the targets of toxic agents that can comprise organisms, macromolecules, or organic or inorganic molecules. A cell-based approach to toxin detection, classification, and identification would exploit the sensitive and specific molecular detection and amplification system developed by cells to sense minute changes in their external milieu. By combining the evolved sensing capability of cells with the luminescent reporter molecules and assays described herein, intracellular molecular and chemical events caused by toxic agents can be converted into detectable spatial and temporal luminescent signals.

When a toxin interacts with a cell, whether it is at the cell surface or within a specific intracellular compartment, the toxin invariably undermines one or more components of the molecular pathways active within the cell. Because the cell is comprised of complex networks of interconnected molecular pathways, the effects of a toxin will likely be transmitted throughout many cellular pathways. Therefore, our strategy is to use molecular markers within key pathways likely to be affected by toxins, including but not limited to cell stress pathways, metabolic pathways, signaling pathways, and growth and division pathways.

We have developed and characterized three classes of cell based luminescent reporter molecules to serve as reporters of toxic threat agents. These 3 classes are as follows:

- (1) *Detectors*: general cell stress detection of a toxin;
- (2) *Classifiers*: perturbation of key molecular pathway(s) for detection and classification of a toxin; and
- 5 (3) *Identifiers*: activity mediated detection and identification of a toxin or a group of toxins.

Thus, in another aspect of the present invention, living cells are used as biosensors to interrogate the environment for the presence of toxic agents. In one embodiment of this aspect, an automated method for cell based toxin characterization is disclosed that comprises providing an array of locations containing cells to be treated 10 with a test substance, wherein the cells possess at least a first luminescent reporter molecule comprising a detector and a second luminescent reporter molecule selected from the group consisting of a classifier or an identifier; contacting the cells with the test substance either before or after possession of the first and second luminescent reporter molecules by the cells; imaging or scanning multiple cells in each of the 15 locations containing multiple cells to obtain luminescent signals from the detector; converting the luminescent signals from the detector into digital data to automatically measure changes in the localization, distribution, or activity of the detector on or in the cell, which indicates the presence of a toxin in the test substance; selectively imaging or scanning the locations containing cells that were contacted with test sample indicated to 20 have a toxin in it to obtain luminescent signals from the second reporter molecule; converting the luminescent signals from the second luminescent reporter molecule into digital data to automatically measure changes in the localization, distribution, or activity of the classifier or identifier on or in the cell, wherein a change in the localization, distribution, structure or activity of the classifier identifies a cell pathway 25 that is perturbed by the toxin present in the test substance, or wherein a change in the localization, distribution, structure or activity of the identifier identifies the specific toxin that is present in the test substance. In a preferred embodiment, the cells possess at least a detector, a classifier, and an identifier. In a further preferred embodiment, the digital data derived from the classifier is used to determine which identifier(s) to 30 employ for identifying the specific toxin or group of toxins.

As used herein, the phrase "the cells possess one or more luminescent reporter molecules" means that the luminescent reporter molecule may be expressed as a

luminescent reporter molecule by the cells, added to the cells as a luminescent reporter molecule, or luminescently labeled by contacting the cell with a luminescently labeled molecule that binds to the reporter molecule, such as a dye or antibody, that binds to the reporter molecule. The luminescent reporter molecule can be expressed or added to the
5 cell either before or after treatment with the test substance.

The luminescent reporters comprising detectors, classifiers, and identifiers may also be distributed separately into single or multiple cell types. For example, one cell type may contain a toxin detector, which, when activated by toxic activity, implies to the user that the same toxin sample should be screened with reporters of the classifier
10 or identifier type in yet another population of cells identical to or different from the cells containing the toxin detector.

The detector, classifier, and identifier can comprise the same reporter molecule, or they can comprise different reporters.

Screening for changes in the localization, distribution, structure or activity of
15 the detectors, classifiers, and/or identifiers can be carried out in either a high throughput or a high content mode. In general, a high-content assay can be converted to a high-throughput assay if the spatial information rendered by the high-content assay can be recoded in such a way as to no longer require optical spatial resolution on the cellular or subcellular levels. For example, a high-content assay for microtubule
20 reorganization can be carried out by optically resolving luminescently labeled cellular microtubules and measuring their morphology (e.g., bundled vs. non-bundled or normal). A high-throughput version of a microtubule reorganization assay would involve only a measurement of total microtubule polymer mass after cellular extraction with a detergent. That is, destabilized microtubules, being more easily extracted, would
25 result in a lower total microtubule mass luminescence signal than unperturbed or drug-stabilized luminescently labeled microtubules in another treated cell population. The luminescent signal emanating from a domain containing one or more cells will therefore be proportional to the total microtubule mass remaining in the cells after toxin treatment and detergent extraction.

30 The methods for detecting, classifying, and identifying toxins can utilize the same screening methods described throughout the instant application, including but not limited to detecting changes in cytoplasm to nucleus translocation, nucleus or nucleolus

to cytoplasm translocation, receptor internalization, mitochondrial membrane potential, signal intensity, the spectral response of the reporter molecule, phosphorylation, intracellular free ion concentration, cell size, cell shape, cytoskeleton organization, metabolic processes, cell motility, cell substrate attachment, cell cycle events, and 5 organellar structure and function.

In all of these embodiments, the methods can be operated in both toxin-mimetic and toxin-inhibitory modes.

Such techniques to assess the presence of toxins are useful for methods including, but not limited to, monitoring the presence of environmental toxins in test 10 samples and for toxins utilized in chemical and biological weapons; and for detecting the presence and characteristics of toxins during environmental remediation, drug discovery, clinical applications, and during the normal development and manufacturing process by virtually any type of industry, including but not limited to agriculture, food processing, automobile, electronic, textile, medical device, and petroleum industries.

15 We have developed and characterized examples of luminescent cell-based reporters, distributed across the 3 sensor classes. The methods disclosed herein can be utilized in conjunction with computer databases, and data management, mining, retrieval, and display methods to extract meaningful patterns from the enormous data set generated by each individual reporter or a combinatorial of reporters in response to 20 toxic agents. Such databases and bioinformatics methods include, but are not limited to, those disclosed in U.S. Patent Application Nos. 09/437,976, filed November 10, 1999; 60/145,770 filed July 27, 1999 and U.S. Patent Application Serial No. to be assigned, filed February 19, 2000. (98,068-C)

Any cell type can be used to carry out this aspect of the invention, including 25 prokaryotes such as bacteria and archaebacteria, and eukaryotes, such as single celled fungi (for example, yeast), molds (for example, Dictyostelium), and protozoa (for example, Euglena). Higher eukaryotes, including, but not limited to, avian, amphibian, insect, and mammalian cells can also be used.

30

Examples of Biosensors

Number	Name	Class	Cell Types	Response to model toxins
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				Positive	Negative
1	Mitochondrial Potential [Donnan Equilibrium Dye]	D	<ul style="list-style-type: none"> LLCPK (pig epithelia) Rat primary hepatocytes 	Valinomycin (10 nM-100 μM) FCCP (10 nM-100 μM)	Oligomycin (10 nM)
2	Heat Shock Protein (Hsp 27, Hsp 70) GFP-chimera	D	<ul style="list-style-type: none"> HeLa 3T3 	Cadmium (10mM)	TNF- α (100ng/ml)
3	Tubulin-cytoskeleton [β -tubulin-GFP chimera]	C	<ul style="list-style-type: none"> BHK HeLa LLCPK 	Paclitaxel (10 nM-20μM) Curacin-A (5 nM-10μM) Nocadazole (7 nM-12μM) Colchicine (5 nM-10μM) Vinblastine (5 nM-10μM)	Staurosporine (1 nM-1 μM)
4	pp38 MAPK- stress signaling [antibody and GFP-chimera]	C	<ul style="list-style-type: none"> 3T3 LLCPK 	Anisomycin (100 μM) Cadmium (10 μM)	TNF- α (100 ng/ml)
5	NF- κ B- stress signaling [antibody and GFP-chimera]	C	<ul style="list-style-type: none"> HeLa 3T3 BHK SNB19 HepG2 LLCPK 	TNF- α (100ng/ml-0.38pg/ml) IL-1 (4ng/ml-0.95pg/ml) Nisin (2-1000 μg/ml) Streptolysin (10 μg/ml) Anisomycin (100 μM)	Anisomycin (10 nM-10 μM) Cadmium (1-10 μM) Penitrem A (10 μM) Valinomycin (1 μM)
6	I κ B [complement to NF- κ B]	C	In many cell types		
7	Tetanus Toxin [Protease activity-based sensor]	I	In many cell types		
8	Anthrax LF [Protease activity-based sensor]	I	In many cell types		

Sensor Class: D= Detector of toxins; C= Classifier of toxins; I= Identifier of toxin or group of toxins
 The model toxins can generally be purchased from Sigma Chemical Company (St. Louis, MO)

- 5 **Examples of Detectors:** This class of sensors provides a first line signal that indicates the presence of a toxic agent. This class of sensors provides detection of general cellular stress that requires resolution limited only to the domain over which the measurement is being made, and they are amenable to high content screens as well. Thus, either high throughput or high content screening modes may be used, including but not limited to translocation of heat shock factors from the cytoplasm to the nucleus,
- 10

and changes in mitochondrial membrane potential, intracellular free ion concentration detection (for example, Ca^{2+} ; H^+), general metabolic status, cell cycle timing events, and organellar structure and function.

5 1. *Mitochondrial Potential*

A key to maintenance of cellular homeostasis is a constant ATP energy charge. The cycling of ATP and its metabolites ADP, AMP, inorganic phosphate, and solution-phase protons is continuously adjusted to meet the catabolic and anabolic needs of the cell. Mitochondria are primarily responsible for maintaining a constant energy charge
10 throughout the entire cell. To produce ATP from its constituents, mitochondria must maintain a constant membrane potential within the organelle itself. Therefore, measurement of this electrical potential with specific luminescent probes provides a sensitive and rapid readout of cellular stress.

We have utilized a positively charged cyanine dye, JC-1 (Molecular Probes,
15 Eugene, OR), which diffuses into the cell and readily partitions into the mitochondrial membrane, for measurement of mitochondrial potential. The photophysics of JC-1 are such that when the probe partitions into the mitochondrial membrane and it experiences an electrical potential >140 mV, the probe aggregates and its spectral response is shifted to the red. At membrane potential values <140 mV, JC-1 is primarily
20 monomeric and its spectral response is shifted toward the blue. Therefore, the ratio of two emission wavelengths (645 nm and 530 nm) of JC-1 partitioned into mitochondria provides a sensitive and continuous measure of mitochondrial membrane potential.

We have been making live cell measurements in a high throughput mode as the basis of a generalized indicator of toxic stress. The goal of our initial experiments was
25 to determine the ratio of J-aggregates of JC-1 dye to its monomeric form both before and after toxic stress.

Procedure

1. Cells were plated and cultured up to overnight.
2. Cells were stained with JC-1 (10 $\mu\text{g}/\text{ml}$) for 30 minutes at 37° C in a CO₂ incubator.
- 30 3. Cells were then washed quickly with HBSS at 37°C (2 times, 150 $\mu\text{l}/\text{well}$), the toxins were added if required, and the entire plate was scanned in a plate reader. The JC-1 monomer was measured optimally with a 485 nm excitation/530 nm emission wavelength filter set, and the aggregates were best measured with a 590 nm excitation/645 nm emission wavelength set.

Results

The mitochondrial potential within several types of living cells, and the effects of toxins on the potential were measured using the fluorescence ratio Em 645 (590)/
5 Em 530 (485) (excitation wavelengths in parentheses). For example, we measured the
effect of 10 µM valinomycin on the mitochondrial potential within LLCPK cells (pig
epithelia). Within seconds of treatment, the toxin induced a more rapid and higher
magnitude decrease (an approximately 50% reduction) in mitochondrial potential than
that found in untreated cells. Hepatocytes were also determined to be sensitive to
10 valinomycin, and the changes in mitochondrial potential were nearly complete within
seconds to minutes after addition of various concentrations of the toxin.

These results are consistent with mitochondrial potential being a model
intracellular detector of cell stress. Because these measurements require no spatial
resolution within individual cells, mitochondrial potential measurements can be made
15 rapidly on an entire cell array (e.g. high throughput). This means, for example, that
complex arrays of many cell types can be probed simultaneously and continuously as a
generalized toxic response. Such an indicator can provide a first line signal to indicate
that a general toxic stress is present in a sample. Further assays can then be conducted
to more specifically identify the toxin using cells classifier or identifier type reporter
20 molecules.

2. Heat Shock Proteins

Most mammalian cells will respond to a variety of environmental stimuli with
the induction of a family of proteins called stress proteins. Anoxia, amino acid
25 analogues, sulfhydryl-reacting reagents, transition metal ions, decouplers of oxidative
phosphorylation, viral infections, ethanol, antibiotics, ionophores, non-steroidal
antiinflammatory drugs, thermal stress and metal chelators are all inducers of cell stress
protein synthesis, function, or both. Upon induction, cell stress proteins play a role in
folding and unfolding proteins, stabilizing proteins in abnormal configurations, and
30 repairing DNA damage.

There is evidence that at least four heat shock proteins translocate from the
cytoplasm to the nucleus upon stress activation of the cell. These proteins include the

heat shock proteins HSP27 and HSP70, the heat shock cognate HSC70, and the heat shock transcription factor HSF1. Therefore, measurement of cytoplasm to nuclear translocation of these proteins (and other stress proteins that translocate from the cytoplasm to the nucleus upon a cell stress) will provide a rapid readout of cellular
5 stress.

We have tested the response of an HSP27-GFP biosensor (SEQ ID 169-170) in two cell lines (BHK and HeLa) using a library of heavy metal chemical compounds as biological toxin stimulants to stress the cells. Briefly, cells expressing the HSP27-GFP biosensor are plated into 96-well microplates, and allowed to attach. The cells are then
10 treated with a panel of cell stress-inducing compounds. Exclusively cytoplasmic localization of the fusion protein was found in unstimulated cells.

Other similar heat shock protein biosensors (HSP-70, HSC70, and HSF1 fused to GFP) can be used as detectors, and are shown in SEQ ID NO: 171-176.

15

Examples of Classifiers:

This class of sensors detects the presence of, and further classifies toxins by identifying the cellular pathway(s) perturbed by the toxin. As such, this suite of sensors can detect and/or classify toxins into broad categories, including but not limited to
20 "toxins affecting signal transduction," "toxins affecting the cytoskeleton," and "toxins affecting protein synthesis". Either high throughput or high content screening modes may be used. Classifiers can comprise compounds including but not limited to tubulin, microtubule-associated proteins, actin, actin-binding proteins including but not limited to vinculin, α -actinin, actin depolymerizing factor/cofilin, profilin, and myosin; NF- κ B,
25 I κ B, GTP-binding proteins including but not limited to rac, rho, and cdc42, and stress-activated protein kinases including but not limited to p38 mitogen-activated protein kinase.

1. Tubulin-cytoskeleton

30 The cell cytoskeleton plays a major role in cellular functions and processes, such as endo- and exocytosis, vesicle transport, and mitosis. Cytoskeleton-affecting

toxins, of proteinaceous and non-proteinaceous form, such as C2 toxin, and several classes of enterotoxins, act either directly on the cytoskeleton, or indirectly via regulatory components controlling the organization of the cytoskeleton. Therefore, measurement of structural changes in the cytoskeleton can provide classification of the
5 toxin into a class of cytoskeleton-affecting toxins. This assay can be conducted in a high content mode, as described previously, or in a high throughput mode. For high throughput as discussed previously.

Such measurements will be valuable for identification of toxins including, but not limited to anti-microtubule agents, agents that generally affect cell cycle
10 progression and cell proliferation, intracellular signal transduction, and metabolic processes.

For microtubule disruption assays, LLCPK cells stably transfected with a tubulin-GFP biosensor plasmid were plated on 96 well cell culture dishes at 50-60% confluence and cultured overnight at 37 °C, 5% CO₂. A series of concentrations (10–
15 500 nM) of 5 compounds (paclitaxel, curacin A, nocodazole, vinblastine, and colchicine) in normal culture media were freshly prepared from stock, and were added to cell culture dishes to replace the old culture media. The cells were then observed with the cell screening system described above, at a 12 hour time point.

Our data indicate that the tubulin chimera localizes to and assembles into
20 microtubules throughout the cell. The microtubule arrays in cells expressing the chimera respond as follows to a variety of anti-microtubule compounds:

	<u>Drug</u>	<u>Response</u>
25	Vinblastine	Destabilization
	Nocodazole	Destabilization
	Paclitaxel	Stabilization
	Colchicine	Destabilization
	Curacin A	Destabilization

Similar data were obtained using cells expressing the tubulin biosensor that
30 were patterned onto cell arrays (such as those described in U.S. Patent Application Serial No. 08/865,341 filed May 29, 1997, incorporated by reference herein in its entirety) and dosed as above.

2. NF-κB

NF-κB is cytoplasmic at basal levels of stimulation, but upon insult translocates to the nucleus where it binds specific DNA response elements and activates transcription of a number of genes. Translocation occurs when IκB is degraded by the proteosome in response to specific phosphorylation and ubiquitination events. IκB normally retains NF-κB in the cytoplasm via direct interaction with the protein, and masking of the NLS sequence of NF-κB. Therefore, although not the initial or defining event of the whole signal cascade, NF-κB translocation to the nucleus can serve as an indicator of cell stress.

We have generated an NF-κB-GFP chimera for analysis in live cells. This was accomplished using standard polymerase chain reaction techniques using a characterized NF-κB p65 cDNA purchased from Invitrogen (Carlsbad, CA) fused to an EYFP PCR amplimer that was obtained from Clontech Laboratories (Palo Alto, CA). The resulting chimera is shown in SEQ ID NO:177-178. The two PCR products were ligated into an eukaryotic expression vector designed to produce the chimeric protein at high levels using the ubiquitous CMV promoter.

NF-κB immunolocalization

For further studies, we characterized endogenous NF-κB activation by immunolocalization in toxin treated cells. The NF-κB antibodies used in this study were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA), and secondary antibodies are from Molecular Probes (Eugene, OR).

For the 3T3 and SNB19 cell types, we determined the effective concentrations that yield response levels of 50% of the maximum (EC50), expressed in units of mass per volume (ng/ml) and units of molarity. Based on molecular weights of 17 kD for both TNF α and IL-1 α , the EC50 levels for these two compounds with 3T3 and SNB19 cell types are given in units of molarity in Table 1. Our results demonstrated reproducibility of the relative responses from zero to maximum dose, but from sample to sample there have been occasional shifts in the baseline intensities of the response at zero concentration.

For these experiments, either 10 or 100 TNF α -treated 3T3 or SNB19 cells/well were tested. On the basis of the standard deviations measured for these samples, and by taking t-values for the student's t-test, we have estimated the minimum detectable doses for each case of cell type, compound, number of cells per well, and for different choices of how many wells are sampled per condition. The latter factor determines the number of degrees of freedom that are provided in the sample of data. Increasing the number of wells from 4 to 16, and increasing the number of cells per well from 10 to 100, improves the minimum detectable doses considerably. For 3T3 cells, which show lower minimum detectable doses than the SNB19 cells, and for the case of 1% false negative and 1% false positive rates, we estimate that 100 cells per well and a sampling of 12 or 16 wells are sufficient to detect a dose approximately equal to the EC50 value of 0.15 ng/ml. If the false positive rate is relaxed to 20%, a concentration of approximately half that value can be detected (0.83 ng/ml). One hundred cells can conveniently be sampled over a cell culture surface area of less than 1 mm².

15

Table 1. EC50 levels for TNF α and IL-1 α (based on molecular weights of 17 kD for both)

Compound	Cell Type	EC50 (10^{-12} moles/liter)
TNF α	3T3	8.8
	SNB19	5.9
IL-1 α	3T3	0.24
	SNB19	59

20

3. Phospho-p38 Mitogen Activated Protein Kinase (pp38MAPK)

MAPKs play a role in not only cell growth and division, but as mediators of cellular stress responses. One MAPK, p38, is activated by chemical stress inducers such as hyper-osmolar sorbitol, hydrogen peroxide, arsenite, cadmium ions, 25 anisomycin, sodium salicylate, and LPS. Activation of p38 is also accompanied by its translocation into the nucleus from the cytoplasm.

MAPK p38 lies in a pathway that is a cascade of kinases. Thus, p38 is a substrate of one or more kinases, and it acts to phosphorylate one or more substrates in time and space within the living cell.

The assay we present here measures, as one of its parameters, p38 activation
5 using immunolocalization of the phosphorylated form of p38 in toxin-treated cells. The assay was developed to be flexible enough to include the simultaneous measurement of other parameters within the same individual cells. Because the signal transduction pathway mediated by the transcription factor NF- κ B is also known to be involved in the cell stress response, we included the activation of NF- κ B as a second parameter in the
10 same assay.

Our experiments demonstrate an immunofluorescence approach can be used to measure p38 MAPK activation either alone or in combination with NF- κ B activation in the same cells. Multiple cell types, model toxins, and antibodies were tested, and significant stimulation of both pathways was measured in a high-content mode. The
15 phospho-p38 antibodies used in this study were purchased from Sigma Chemical Company (St. Louis, MO). We report that at least two cell stress signaling pathways can not only be measured simultaneously, but are differentially responsive to classes of model toxins. Figure 36 shows the differential response of the p38 MAPK and NF- κ B pathways across three model toxins and two different cell types. Note that when added
20 alone, three of the model toxins (IL1 α , TNF α and Anisomycin) can be differentiated by the two assays as activators of specific pathways.

IkB chimera

IkB degradation is the key event leading to nuclear translocation of NF- κ B and
25 activation of the NF κ B-mediated stress response. We have chosen this sensor to complement the NF- κ B sensor as a *classifier* in a high-throughput mode: the measurement of loss of signal due to degradation of the IkB-GFP fusion protein requires no spatial resolution within individual cells, and as such we envision IkB degradation measurements being made rapidly on an entire cell substrate.

30 This biosensor is based on fusion of the first 60 amino acids of IkB to the Fred25 variant of GFP. SEQ ID 179-180 This region of IkB contains all the regulatory

sequences, including phosphorylation sites and ubiquitination sites, necessary to confer proteosome degradation upon the biosensor. Knowing this, stimulation of any pathway that would typically lead to NFkB translocation results in degradation of this biosensor. Monitoring the fluorescence intensity of cells expressing IkB-GFP identifies the
5 degradation process.

Examples of Identifiers:

In our toxin identification strategy, the first two levels of characterization ensure
10 a rapid readout of toxin class without sacrificing the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. The third level of biosensors are identifiers, which can identify a specific toxin or group of toxins. In one embodiment, an identifier comprises a protease biosensor that responds to the activity of a specific toxin. Other identifiers are produced with reporters/biosensors specific to
15 their activities. These include, but are not limited to post-translational modifications such as phosphorylation or ADP-ribosylation, translocation between cellular organelles or compartments, effects on specific organelles or cellular components (for example, membrane permeabilization, cytoskeleton rearrangement, etc.)

ADP-ribosylating toxins – These toxins include Pseudomonas toxin A, diphtheria
20 toxin, botulinum toxin, pertussis toxin, and cholera toxin. For example, C. botulinum C2 toxin induces the ADP-ribosylation of Arg177 in the cytoskeletal protein actin, thus altering its assembly properties. Besides the construction of a classifier assay to measure actin-cytoskeleton regulation, an identifier assay can be constructed to detect the specific actin ADP-ribosylation. Because the ADP-ribosylation induces a
25 conformational change that no longer permits the modified actin to polymerize, this conformational change can be detected intracellularly in several possible ways using luminescent reagents. For example, actin can be luminescently labeled using a fluorescent reagent with an appropriate excited state lifetime that allows for the measurement of the rotational diffusion of the intracellular actin using steady state
30 fluorescence anisotropy. That is, toxin-modified actin will no longer be able to assemble into rigid filaments and will therefore produce only luminescent signals with

relatively low anisotropy, which can be readily measured with an imaging system. In another embodiment, actin can be labeled with a polarity-sensitive fluorescent reagent that reports changes in actin-conformation through spectral shifts of the attached reagent. That is, toxin-treatment will induce a conformational change in intracellular actin such that a ratio of two fluorescence wavelengths will provide a measure of actin ADP-ribosylation.

5 Cytotoxic phospholipases – Several gram-positive bacterial species produce cytotoxic phospholipases. For example, Clostridium perfringens produces a phospholipase C specific for the cleavage of phosphoinositides. These 10 phosphoinositides (e.g., inositol 1,4,5-trisphosphate) induce the release of calcium ions from intracellular organelles. An assay that can be conducted as either high-content or high-throughput can be constructed to measure the release of calcium ions using fluorescent reagents that have altered spectral properties when complexed with the metal ion. Therefore, a direct consequence of the action of a phospholipase C based 15 toxin can be measured as a change in cellular calcium ion concentration.

10 Exfoliative toxins – These toxins are produced by several Staphylococcal species and can consist of several serotypes. A specific identifier for these toxins can be constructed by measuring the morphological changes in their target organelle, the desmosome, which occur at the junctions between cells. The exfoliative toxins are 20 known to change the morphology of the desmosomes into two smaller components called hemidesmosomes. In the high-content assay for exfoliative toxins, epithelial cells whose desmosomes are luminescently labeled are subjected to image analysis. A method that detects the morphological change between desmosomes and hemidesmosomes is used to quantify the activity of the toxins on the cells.

25 Most of these identifiers can be used in high throughput assays requiring no spatial resolution, as well as in high content assays.

Several biological threat agents act as specific proteases, and thus we have focused on the development of fluorescent protein biosensors that report the proteolytic cleavage of specific amino acid sequences found within the target proteins.

30 A number of such protease biosensors (including FRET biosensors) are disclosed above, such as the caspase biosensors, anthrax, tetanus, Botulinum, and the

zinc metalloproteases. FRET is a powerful technique in that small changes in protein conformation, many of which are associated with toxin activity, can not only be measured with high precision in time and space within living cells, but can be measured in a high-throughput mode, as discussed above.

5 As described above, one of skill in the art will recognize that the protease biosensors of this aspect of the invention can be adapted to report the activity of any protease, by a substitution of the appropriate protease recognition site in any of the constructs (see Figure 29B). As disclosed above, these biosensors can be used in high-content or high throughput screens to detect *in vivo* activation of enzymatic activity by
10 toxins, and to identify specific activity based on cleavage of a known recognition motif. These biosensors can be used in both live cell and fixed end-point assays, and can be combined with additional measurements to provide a multi-parameter assay.

Anthrax LF

15 Anthrax is a well-known agent of biological warfare and is an excellent target for development of a biosensor in the *identifier* class. Lethal factor (LF) is one of the protein components that confer toxicity to anthrax, and recently two of its targets within cells were identified. LF is a metalloprotease that specifically cleaves Mek1 and Mek2 proteins, kinases that are part of the MAP-kinase signaling pathway. Construction of
20 lethal factor protease biosensors are described above. (SEQ ID NO:7-8; 9-10) Green fluorescent protein (GFP) is fused in-frame at the amino terminus of either Mek1 or Mek2 (or both), resulting in a chimeric protein that is retained in the cytoplasm due to the presence of a nuclear export sequence (NES) present in both of the target molecules. Upon cleavage by active lethal factor, GFP is released from the chimera and
25 is free to diffuse into the nucleus. Therefore, measuring the accumulation of GFP in the nucleus provides a direct measure of LF activity on its natural target, the living cell.

30 While a preferred form of the invention has been shown in the drawings and described, since variations in the preferred form will be apparent to those skilled in the art, the invention should not be construed as limited to the specific form shown and described, but instead is as set forth in the claims.

CLAIMS

We claim:

1. An automated method for cell based toxin characterization comprising
 - providing an array of locations containing cells to be treated with a test substance, wherein the cells possess at least a first luminescent reporter molecule comprising a detector and a second luminescent reporter molecule selected from the group consisting of a classifier or an identifier;
 - contacting the cells with the test substance either before or after possession of the first and second luminescent reporter molecules by the cells; wherein the localization, distribution, structure, or activity of the first and second luminescent reporter molecule is modified when the cell is contacted with the toxin,
 - imaging or scanning multiple cells in each of the locations containing multiple cells to obtain luminescent signals from the detector;
 - converting the luminescent signals from the detector into digital data;
- 10 -utilizing the digital data from the detector to automatically measure the localization, distribution, or activity of the detector on or in the cell, wherein a change in the localization, distribution, structure or activity of the detector indicates the presence of a toxin in the test substance;
- 15 -selectively imaging or scanning the locations containing cells that were contacted with test sample indicated to have a toxin in it to obtain luminescent signals from the second reporter molecule;
- 20 -converting the luminescent signals from the second luminescent reporter molecule into digital data;
- 25 -utilizing the digital data from the second luminescent reporter molecule to automatically measure the localization, distribution, or activity of the classifier or identifier on or in the cell, wherein a change in the localization, distribution, structure or activity of the classifier identifies a cell pathway that is perturbed by the toxin present in the test substance, or wherein a change in the localization, distribution, structure or activity of the identifier identifies the specific toxin or group of toxins that are present in the test substance.
- 30

2. The method of claim 1 wherein the second luminescent reporter molecule is a classifier, and the digital data derived from the classifier is used to select an appropriate identifier for identification of the specific toxin or group of toxins.
- 5 3. An automated method for cell based toxin characterization comprising
 - providing an array of locations containing cells to be treated with a test substance, wherein the cells possess at least a first luminescent reporter molecule comprising a detector, a second luminescent reporter molecule comprising a classifier, and a third luminescent reporter molecule comprising an identifier;
 - 10 -contacting the cells with the test substance either before or after possession of the first, second, and third luminescent reporter molecules by the cells; wherein the localization, distribution, structure, or activity of the first, second, and third luminescent reporter molecules is modified when the cell is contacted with the toxin,
 - 15 -imaging or scanning multiple cells in each of the locations containing multiple cells to obtain luminescent signals from the detector;
 - converting the luminescent signals from the detector into digital data;
 - utilizing the digital data from the detector to automatically measure the localization, distribution, or activity of the detector on or in the cell, wherein a change in the localization, distribution, structure or activity of the detector indicates the presence of a toxin in the test substance;
 - 20 -selectively imaging or scanning the locations containing cells that were contacted with test sample indicated to have a toxin in it to obtain luminescent signals from the classifier;
 - converting the luminescent signals from the classifier into digital data;
 - 25 -utilizing the digital data from the classifier to automatically measure the localization, distribution, or activity of the classifier on or in the cell, wherein a change in the localization, distribution, structure or activity of the classifier identifies a cell pathway that is perturbed by the toxin present in the test substance;
 - selectively imaging or scanning the locations containing cells that were contacted with test sample indicated to have a toxin in it to obtain luminescent signals from the identifier;
 - 30 -converting the luminescent signals from the identifier into digital data; and

-utilizing the digital data from the identifier to automatically measure the localization, distribution, or activity of the identifier on or in the cell, wherein a change in the localization, distribution, structure or activity of the identifier identifies the specific toxin or group of toxins that is present in the test substance.

5

4. The method of claim 3 wherein the digital data derived from the classifier is used to select an appropriate identifier for identification of the specific toxin or group of toxins.

10

5. The method of any one of claim 1-4 wherein the detector comprises a molecule selected from the group consisting of heat shock proteins and compounds that respond to changes in mitochondrial membrane potential, intracellular free ion concentration, cytoskeletal organization, general metabolic status, cell cycle timing events, and organellar structure and function.

15

6. The method of any one of claim 1-5 wherein the classifier comprises a molecule selected from the group consisting of tubulin, microtubule-associated proteins, actin, actin-binding proteins, NF- κ B, I κ B, and stress-activated kinases.

20

7. The method of any one of claim 1-6 wherein the cell pathway is selected from the group consisting of cell stress pathways, cell metabolic pathways, cell signaling pathways, cell growth pathways, and cell division pathways.

25

8. The method of claim 1, wherein the second luminescent reporter molecule is an identifier, and the identifier identifies a toxin or group of toxins selected from the group consisting of proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.

30

9. The method of any one of claim 3-7, wherein the identifier identifies a toxin or group of toxins selected from the group consisting of proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.

10. The method of any of claims 1-9 wherein the change in the localization, distribution, structure or activity of the first, second, or third luminescent reporter molecules is selected from the group consisting of cytoplasm to nucleus translocation, nucleus or nucleolus to cytoplasm translocation, receptor internalization, mitochondrial membrane potential, loss of signal, the spectral response of the reporter molecule, phosphorylation, intracellular free ion concentration, cell size, cell shape, cytoskeleton organization, metabolic processes, cell motility, cell substrate attachment, cell cycle events, and organellar structure and function.
5
11. The method of any one of claims 1-10, wherein the imaging or scanning multiple cells in each of the locations containing multiple cells to obtain luminescent signals from the detector is carried out in a high throughput mode.
10
12. The method of any one of claims 1-10, wherein the imaging or scanning multiple cells in each of the locations containing multiple cells to obtain luminescent signals from the detector is carried out in a high content mode.
15
13. The method of claim 1-10 wherein the selective imaging or scanning of the locations containing cells that were contacted with test sample indicated to have a toxin in it to obtain luminescent signals from the second or third reporter molecule is carried out in a high throughput mode.
20
14. The method of claim 1-10 wherein the selective imaging or scanning of the locations containing cells that were contacted with test sample indicated to have a toxin in it to obtain luminescent signals from the second or third reporter molecule is carried out in a high content mode.
25
15. The method of any one of claims 1-14 further comprising providing a digital storage media for data storage and archiving.
30
16. The method of claim 15 further comprising a means for automated control, acquisition, processing and display of results.

17. A computer readable storage medium comprising a program containing a set of instructions for causing a cell screening system to execute the method of any one of claims 1-16, wherein the cell screening system comprises an optical system with a stage
5 adapted for holding a plate containing cells, a means for moving the stage or the optical system, a digital camera, a means for directing light emitted from the cells to the digital camera, and a computer means for receiving and processing the digital data from the digital camera.
- 10 18. A kit for cell based toxin detection comprising:
(a) at least one reporter molecule, wherein the localization, distribution, structure, or activity of the reporter molecule is modified when the cell is contacted with a toxin;
(b) instructions for using the reporter molecule to carry out the method of
15 any one of claims 1-16 to detect toxins in a test substance.
19. The kit of claim 18 further comprising the computer readable storage medium of claim 17.
- 20 20. An automated method for cell based toxin characterization comprising
-providing a first array of locations containing cells to be treated with a test substance, wherein the cells possess at least a first luminescent reporter molecule comprising a reporter molecule selected from the group consisting of detectors and classifiers;
25 -contacting the cells with the test substance either before or after possession of the first luminescent reporter molecule by the cells; wherein the localization, distribution, structure, or activity of the first luminescent reporter molecule is modified when the cell is contacted with the toxin,
-imaging or scanning multiple cells in each of the locations containing multiple
30 cells to obtain luminescent signals from the detector;
-converting the luminescent signals from the detector into digital data;

- utilizing the digital data from the detector to automatically measure the localization, distribution, or activity of the detector on or in the cell, wherein a change in the localization, distribution, structure or activity of the detector indicates the presence of a toxin in the test substance,
- 5 -providing a second array of locations containing cells to be treated with the test substance, wherein the cells possess at least a second luminescent reporter molecule comprising a reporter molecule selected from the group consisting of classifiers and identifiers, and wherein the second array of locations containing cells can comprise either the same or a different cell type as the first array of locations containing cells;
- 10 -contacting the second array of locations containing cells with the test substance either before or after possession of the second luminescent reporter molecule by the cells; wherein the localization, distribution, structure, or activity of the second luminescent reporter molecule is modified when the cell is contacted with the toxin;
- utilizing the digital data from the second luminescent reporter molecule to
- 15 automatically measure the localization, distribution, or activity of the classifier or identifier on or in the cell, wherein a change in the localization, distribution, structure or activity of the classifier identifies a cell pathway that is perturbed by the toxin present in the test substance, or wherein a change in the localization, distribution, structure or activity of the identifier identifies the specific toxin or group of toxins that
- 20 are present in the test substance.

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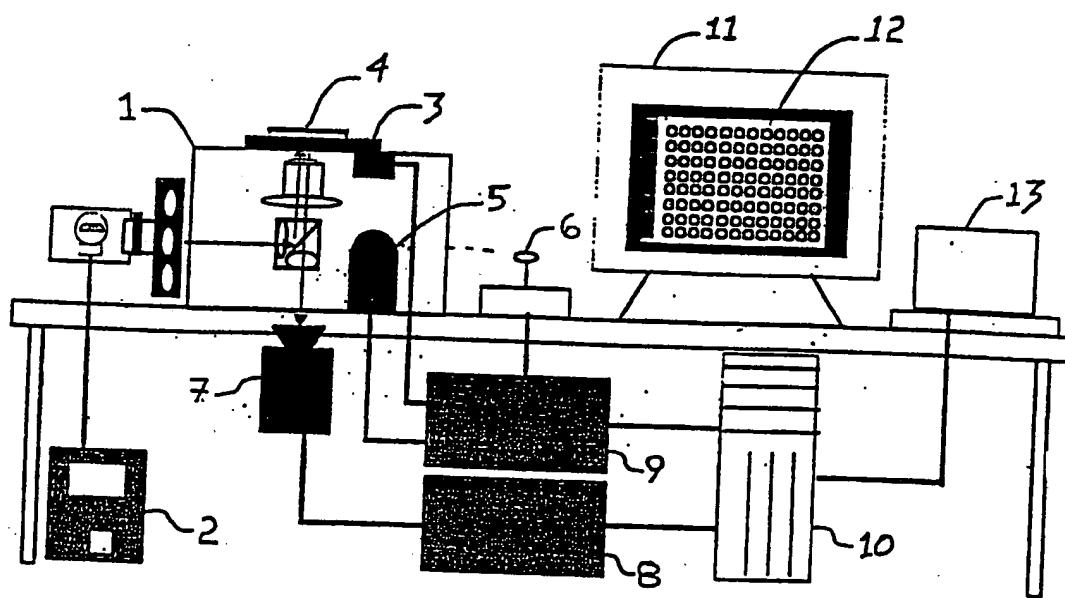
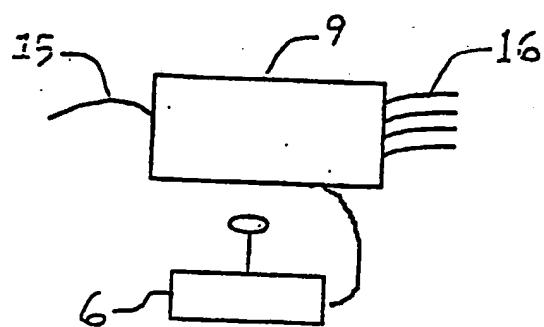
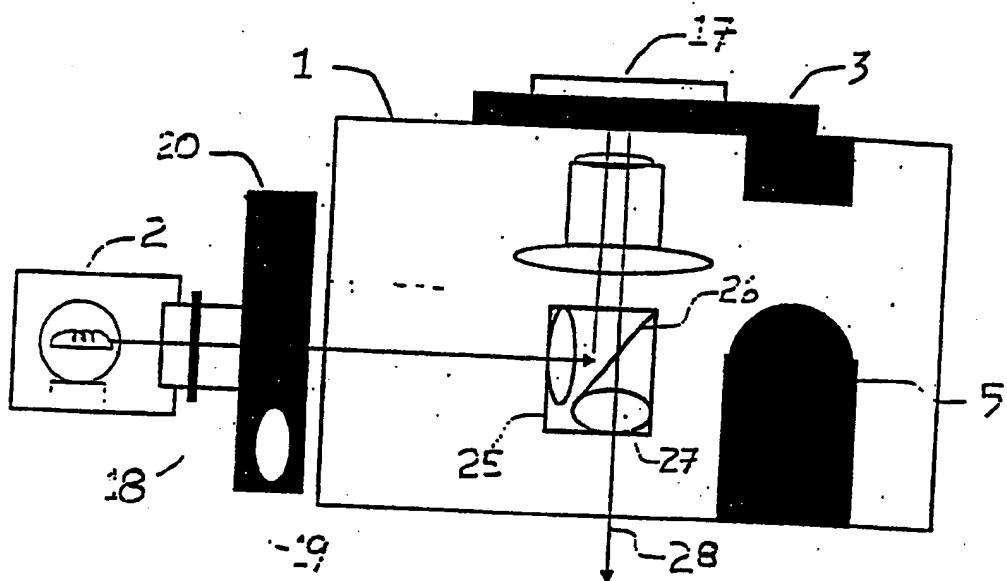


FIGURE 1

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**FIGURE 2**

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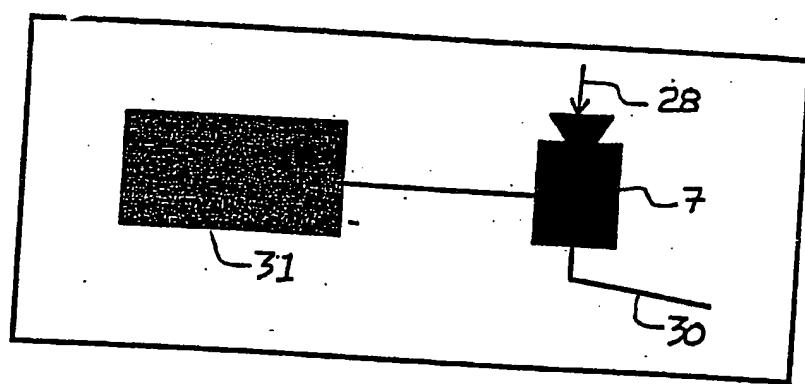


FIGURE 3

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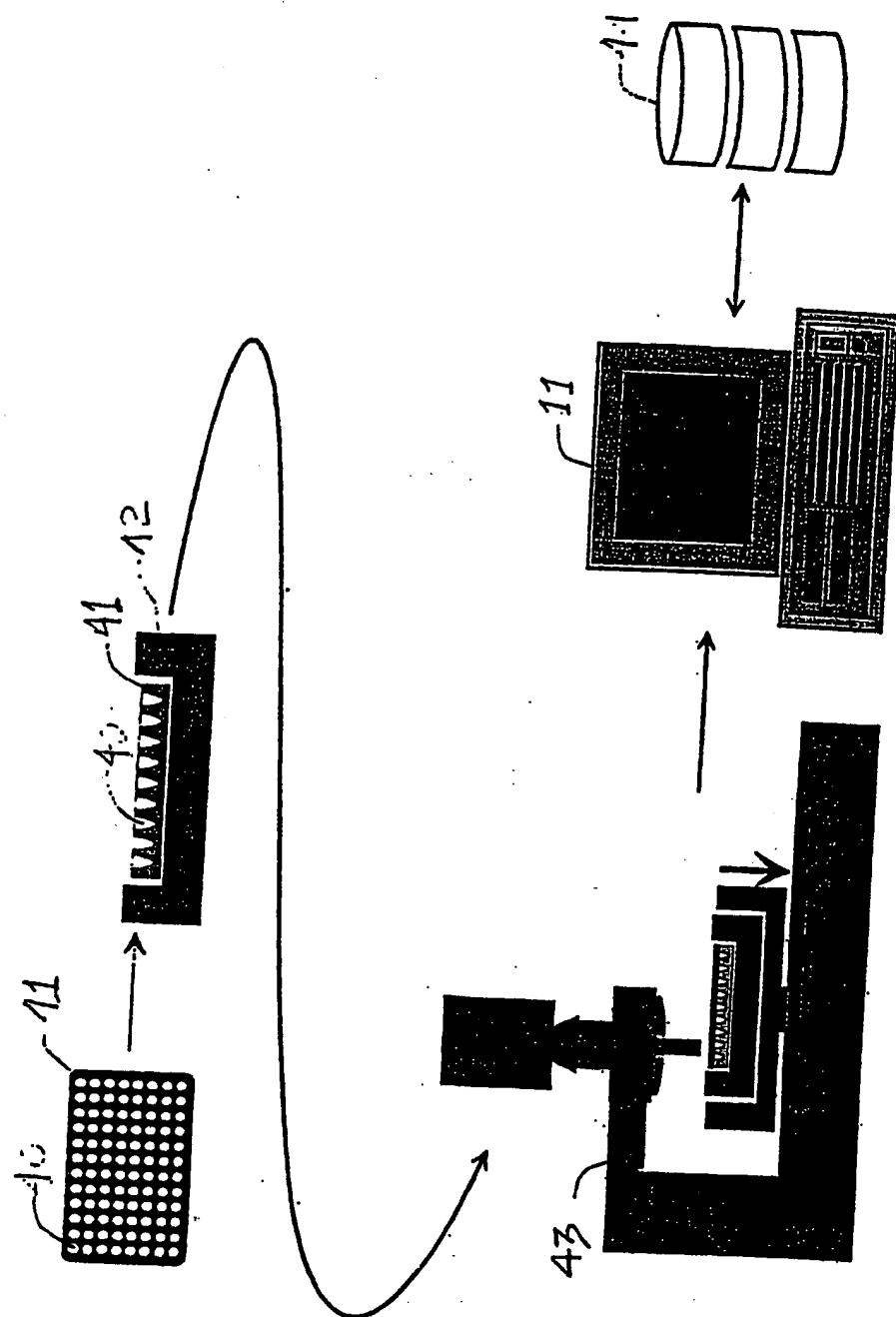


FIGURE 4

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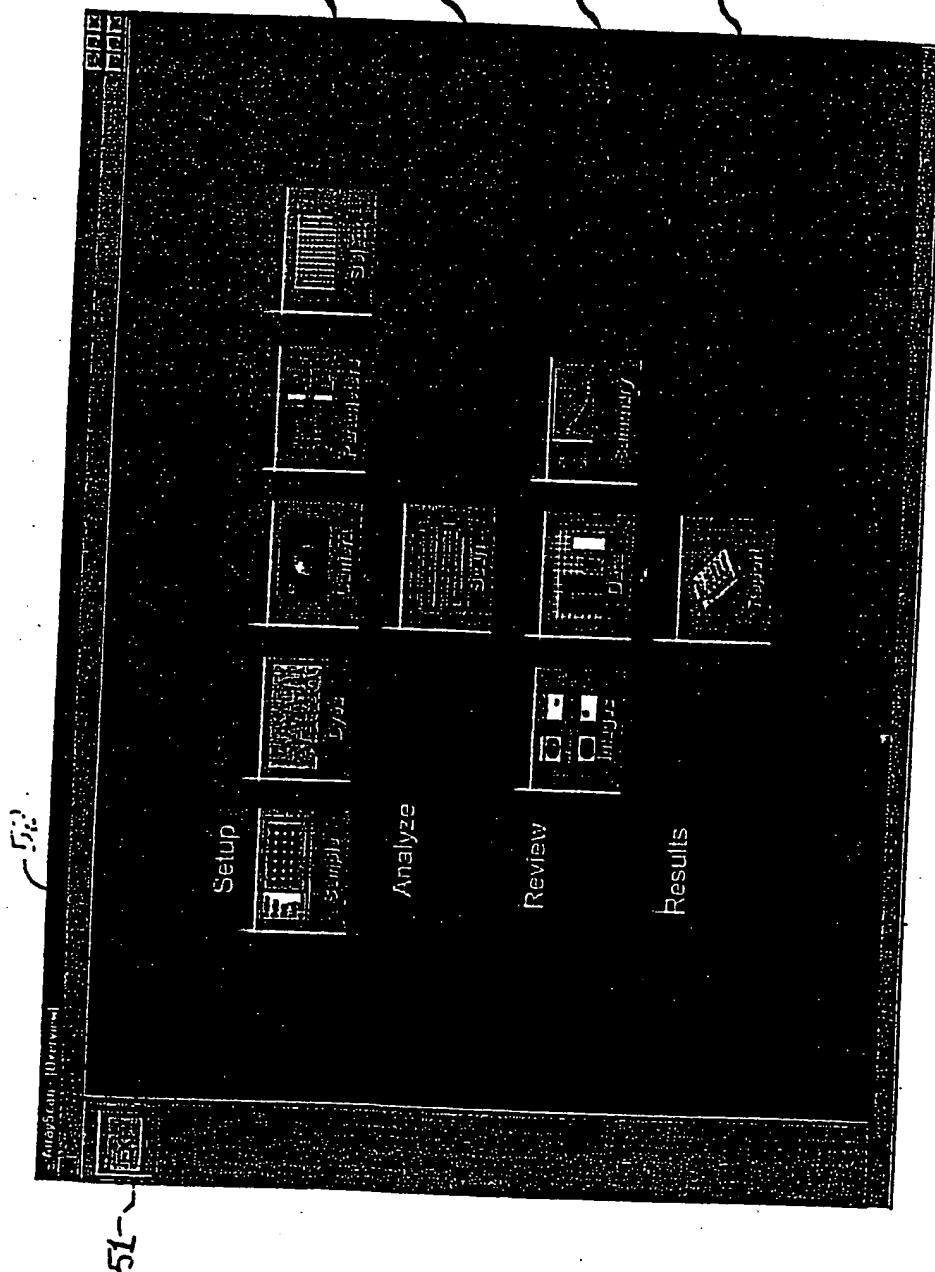
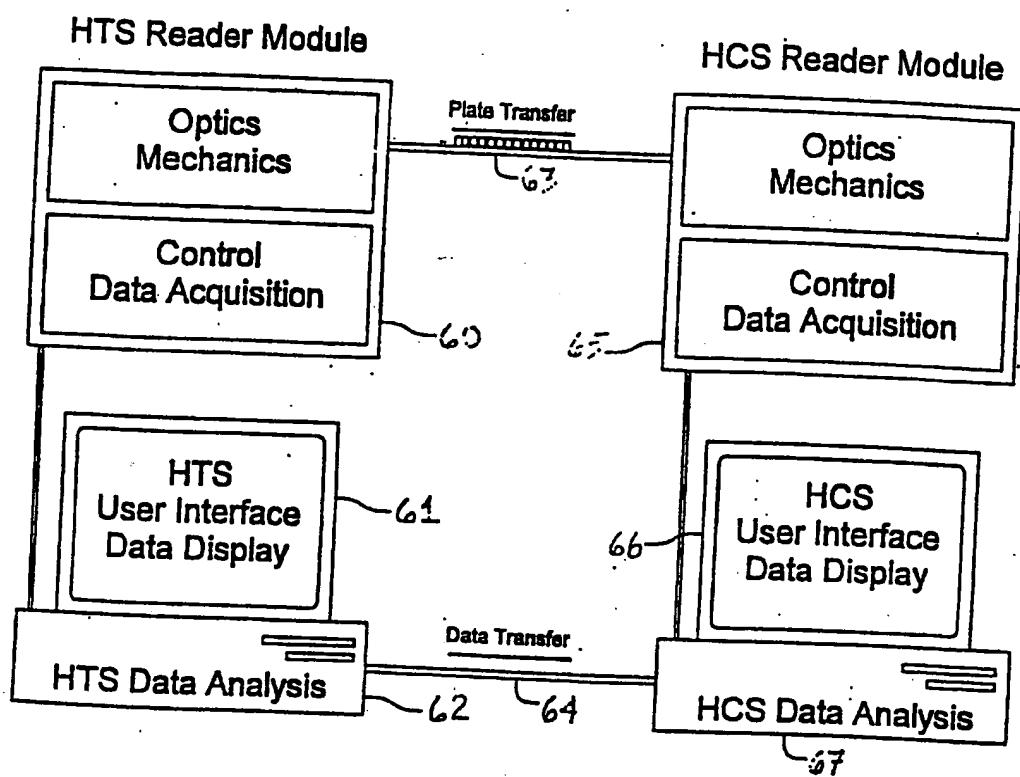


FIGURE 5

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FIG

6

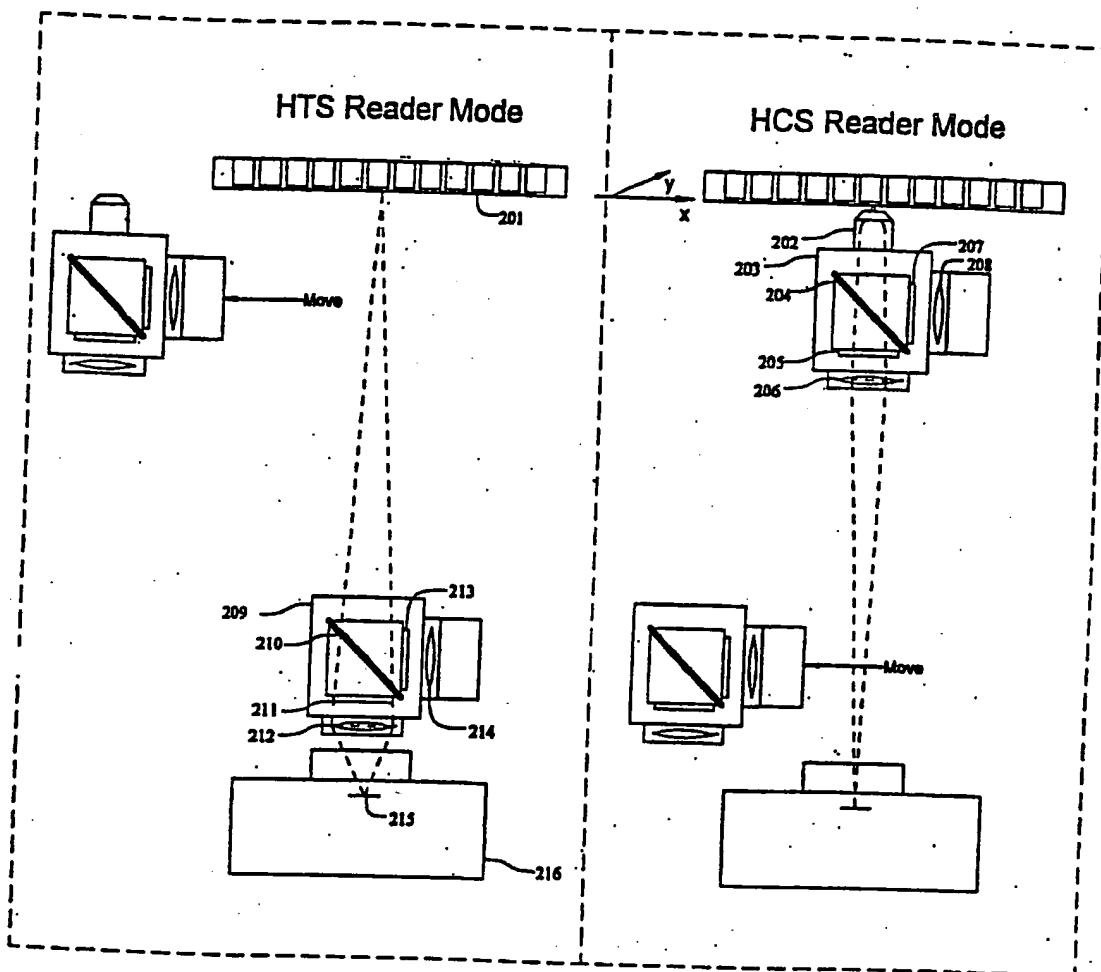


FIGURE 7

Fluid Delivery System for Cell Based Screening System

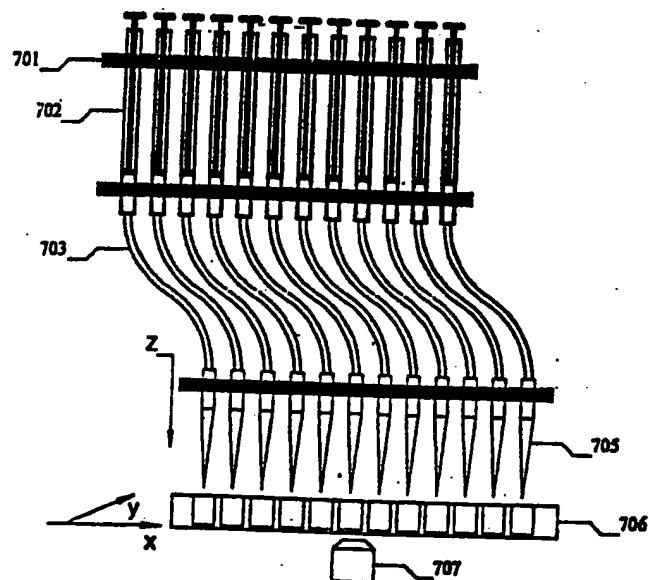
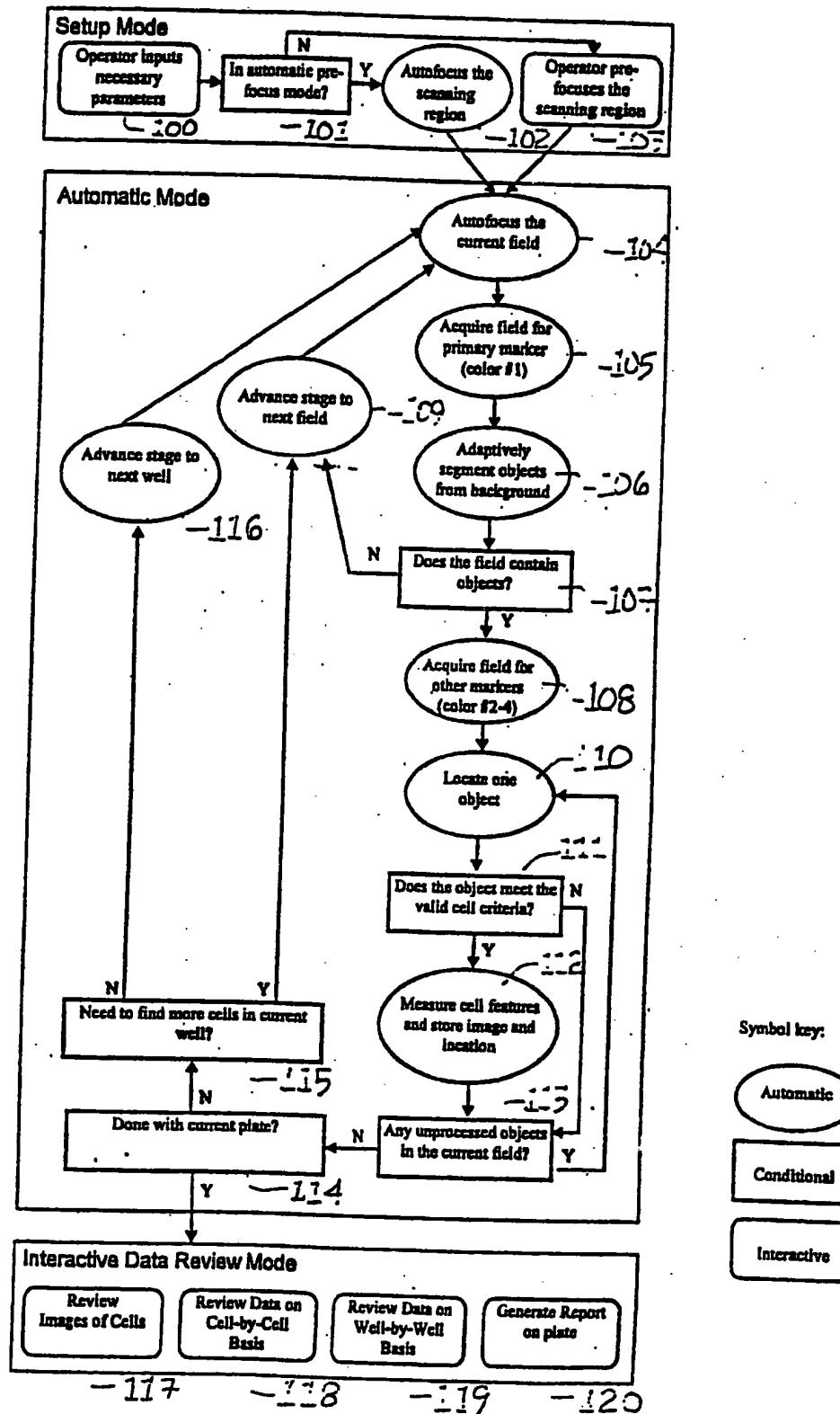


FIGURE 8

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Symbol key:

- Automatic
- Conditional
- Interactive

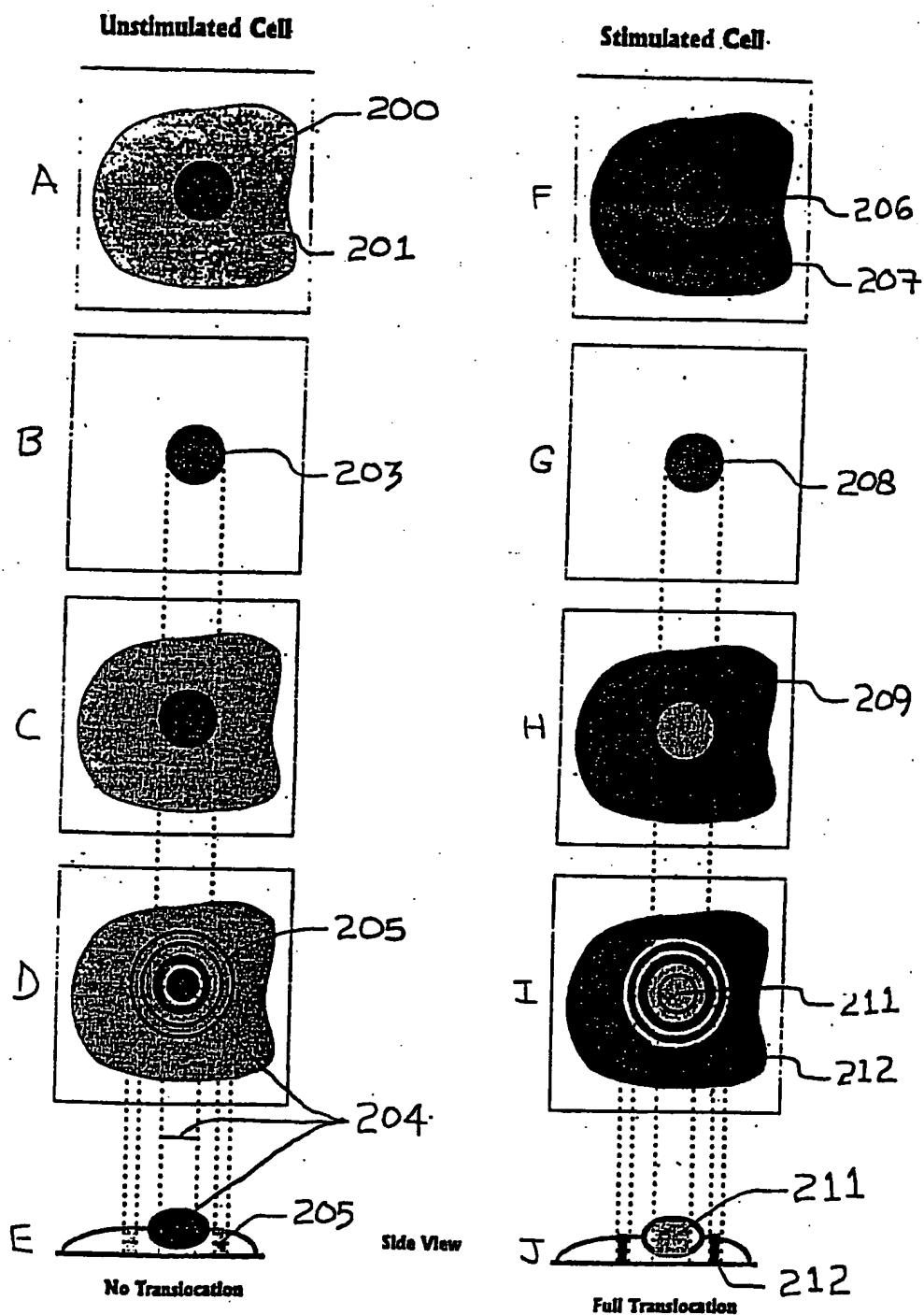
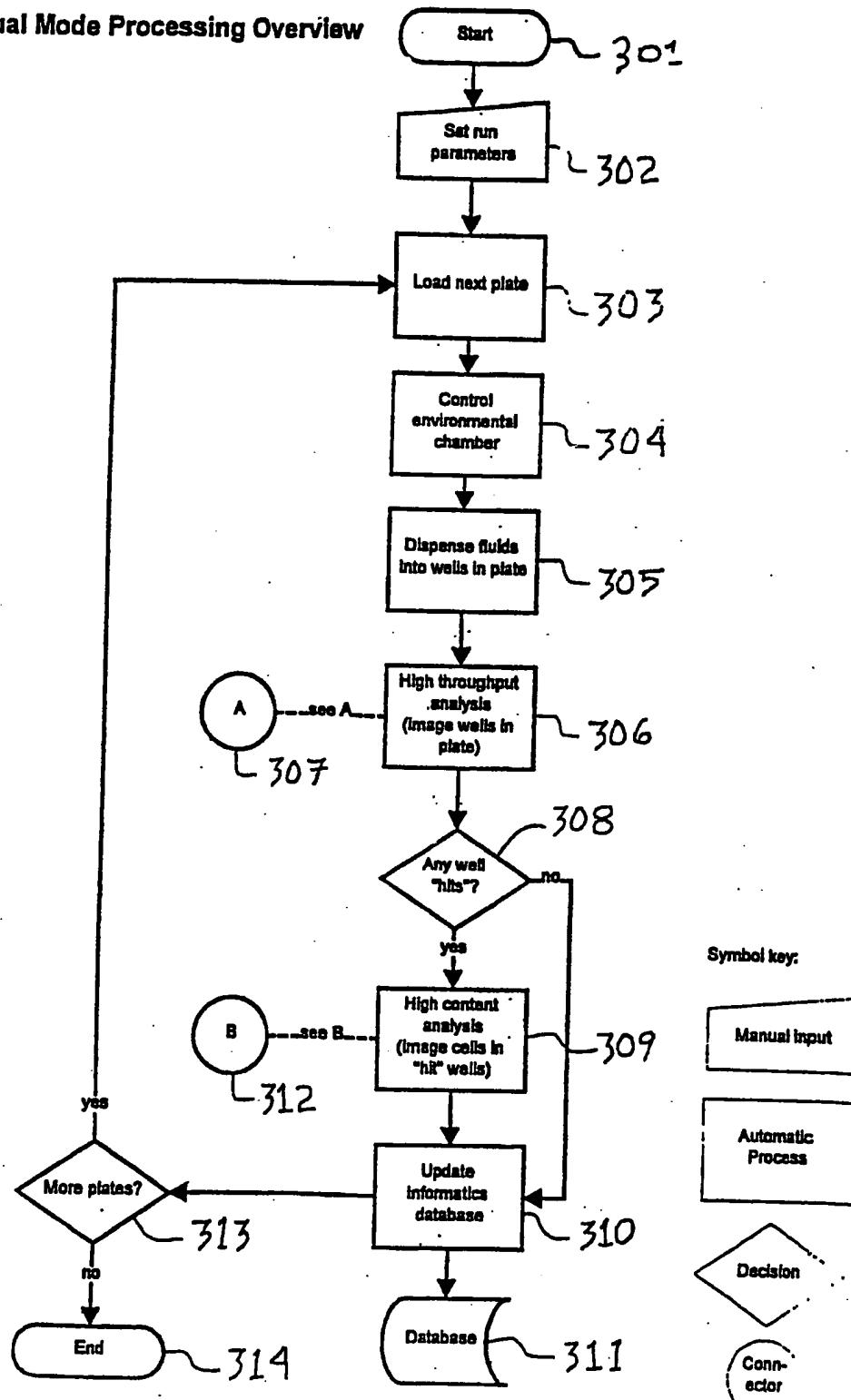
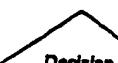
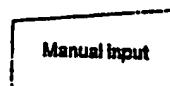


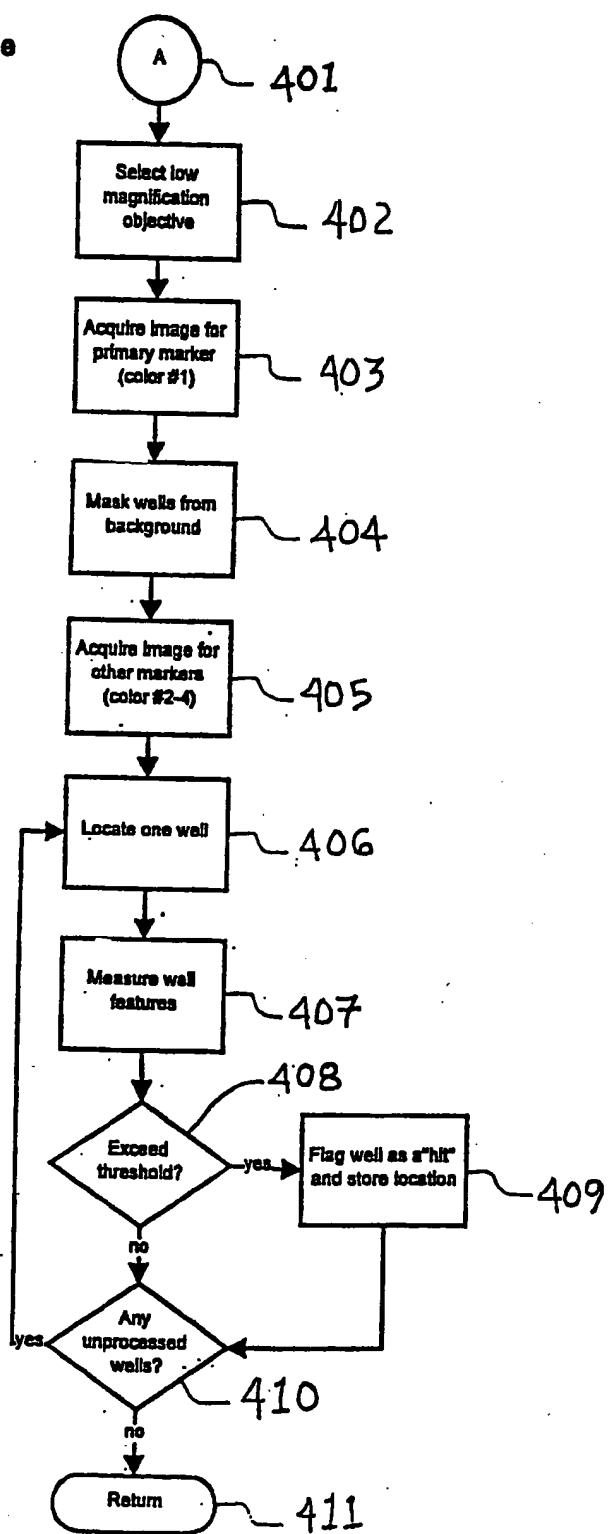
FIGURE 10

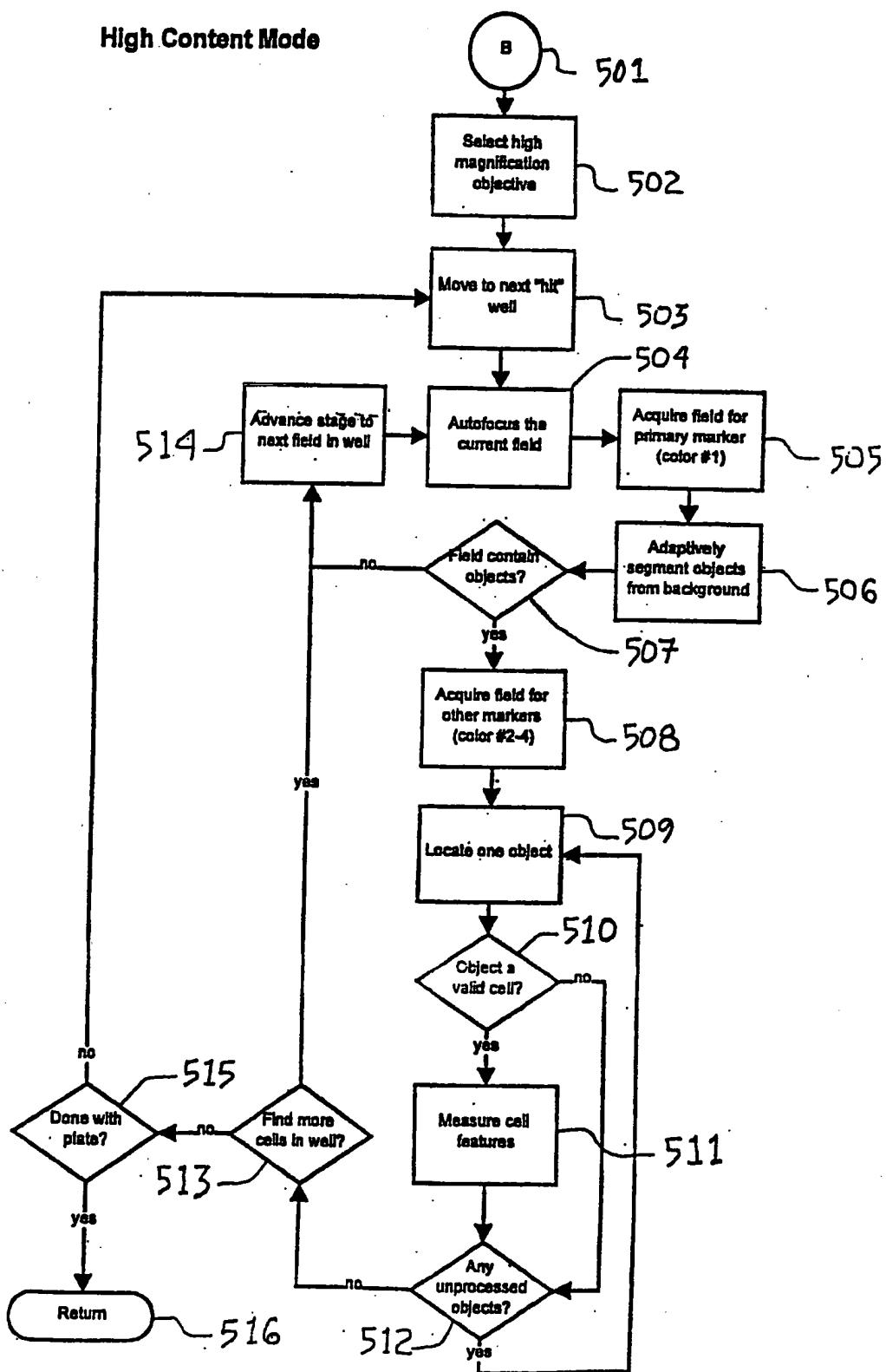
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Dual Mode Processing Overview

Symbol key:



High Throughput Mode

High Content Mode

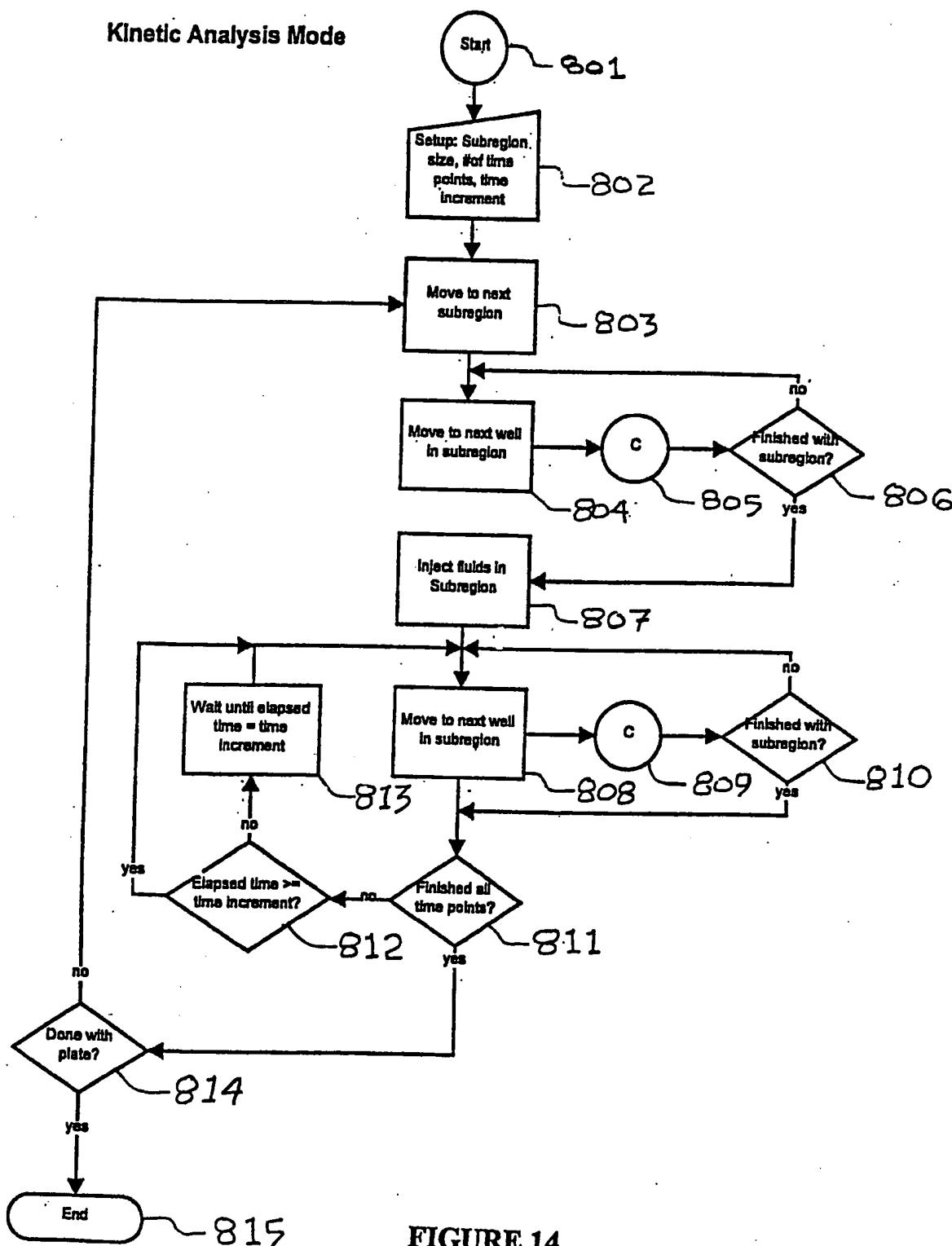
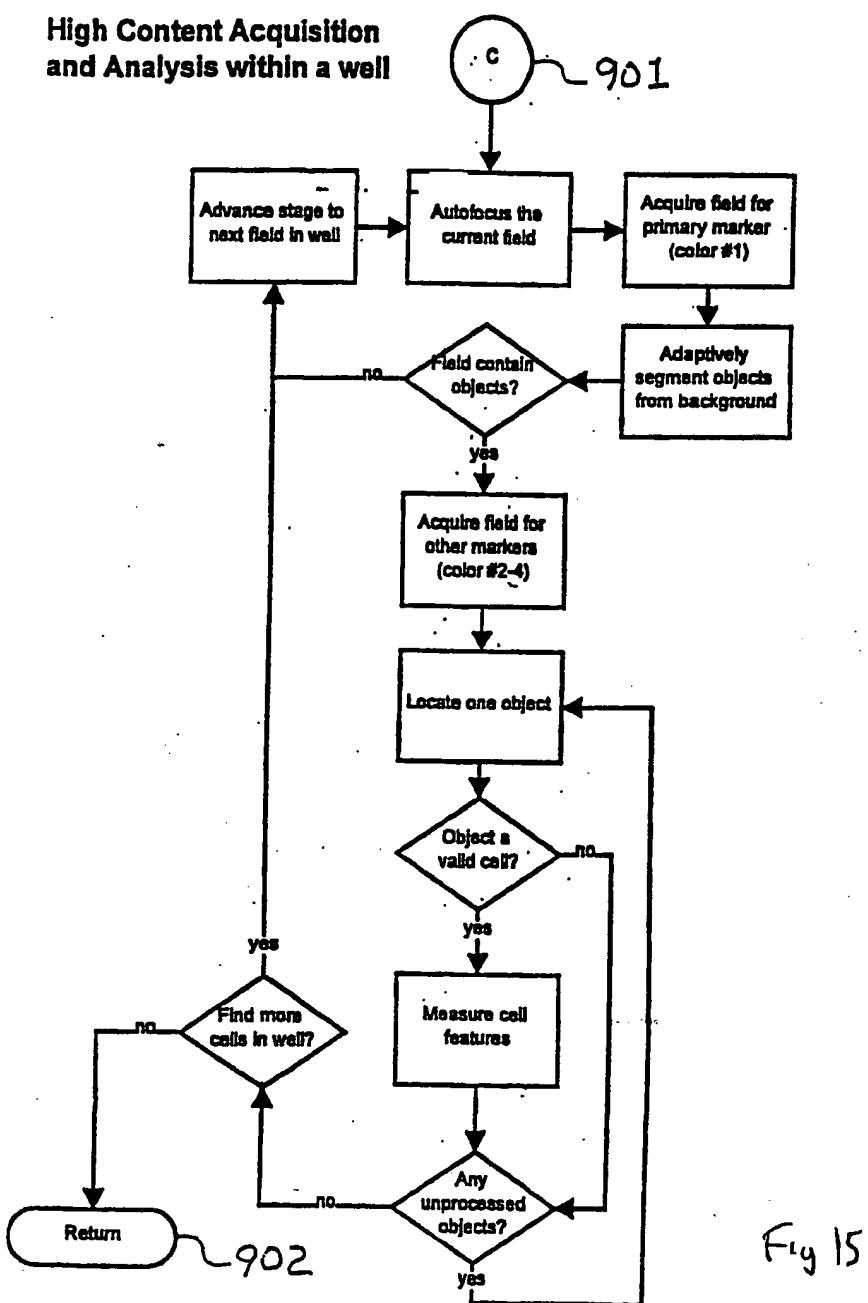


FIGURE 14



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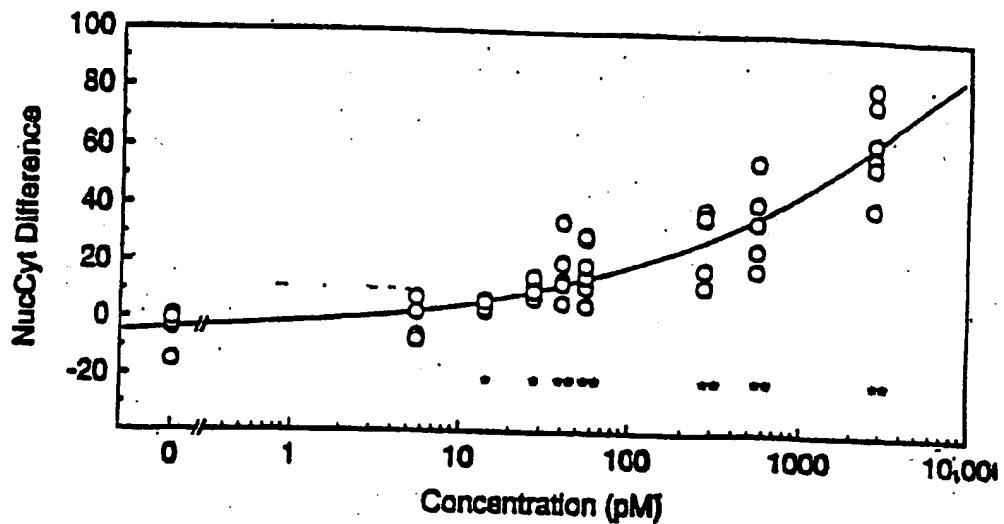


FIGURE 16

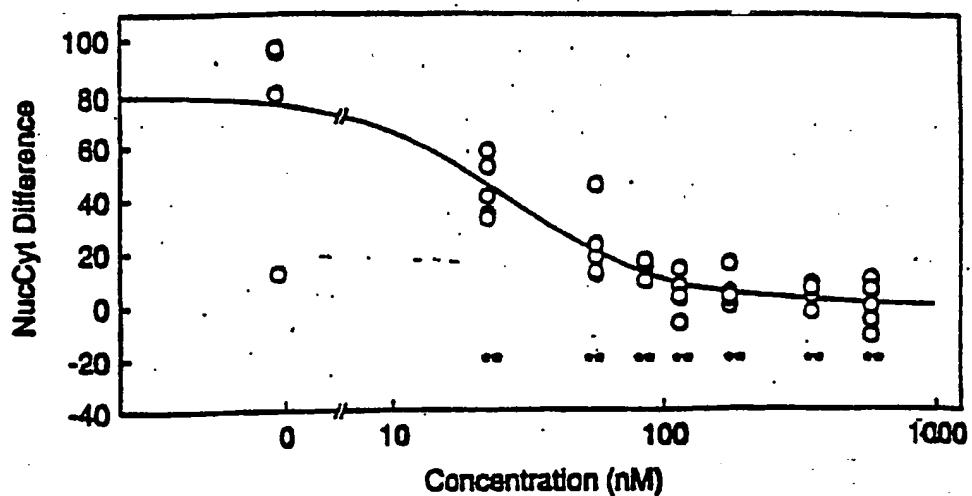


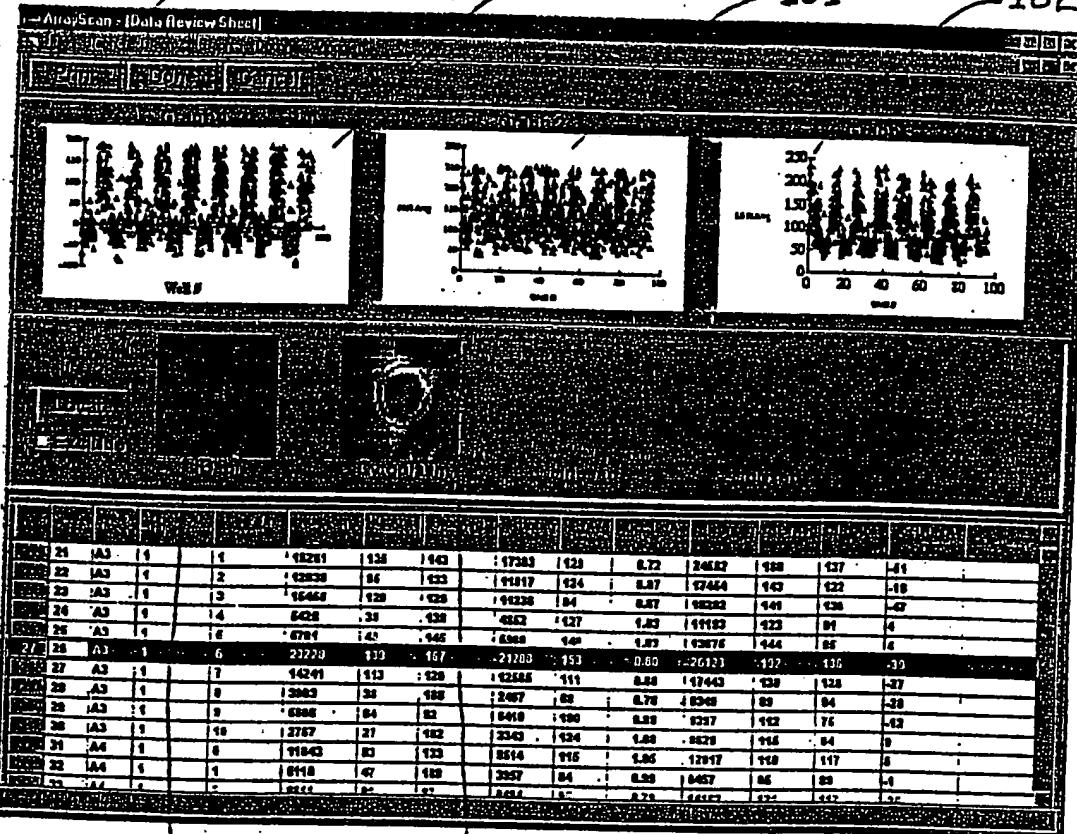
FIGURE 17

. 183

-180

-181

-182

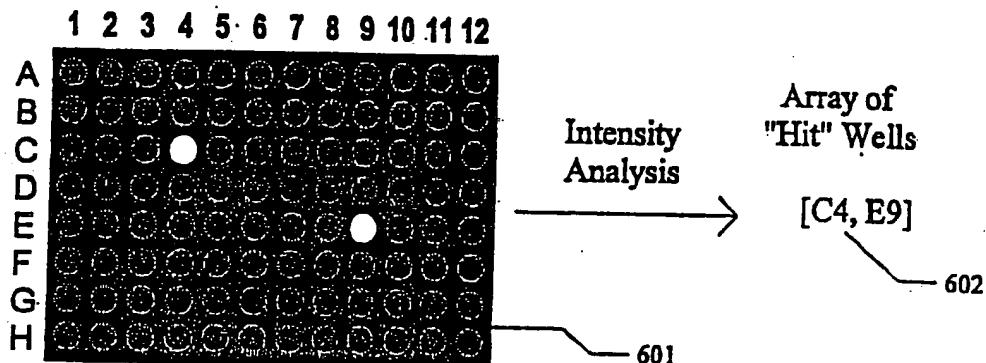


- 184

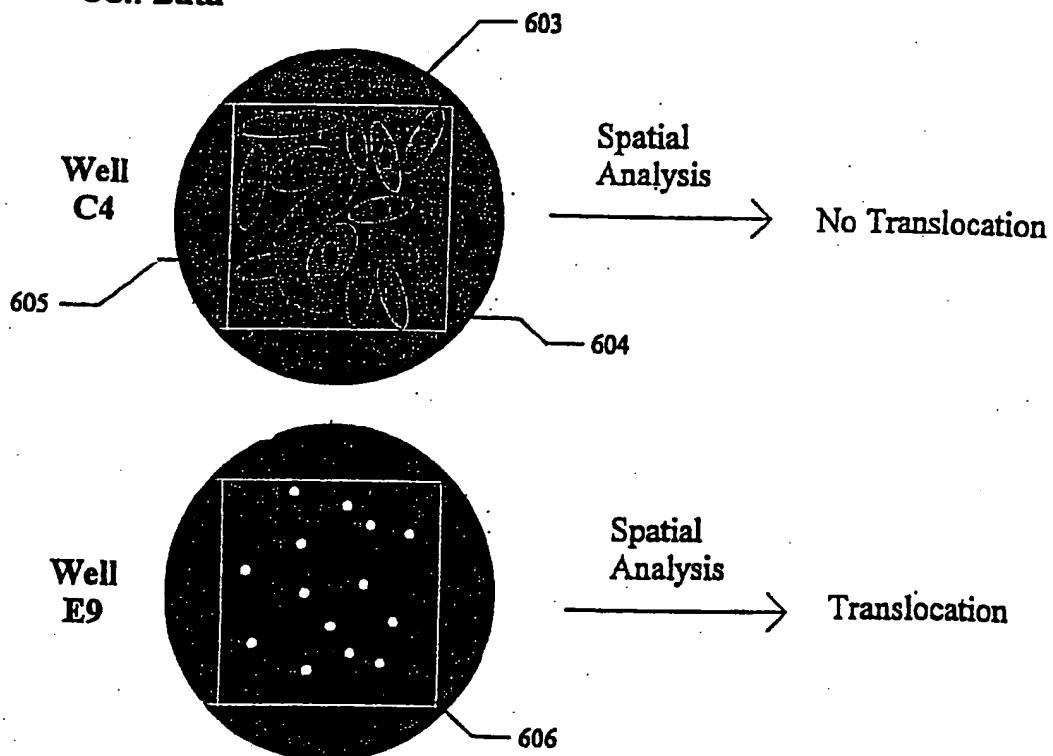
- 185

18

**Low Resolution
Well Data**



**High Resolution
Cell Data**



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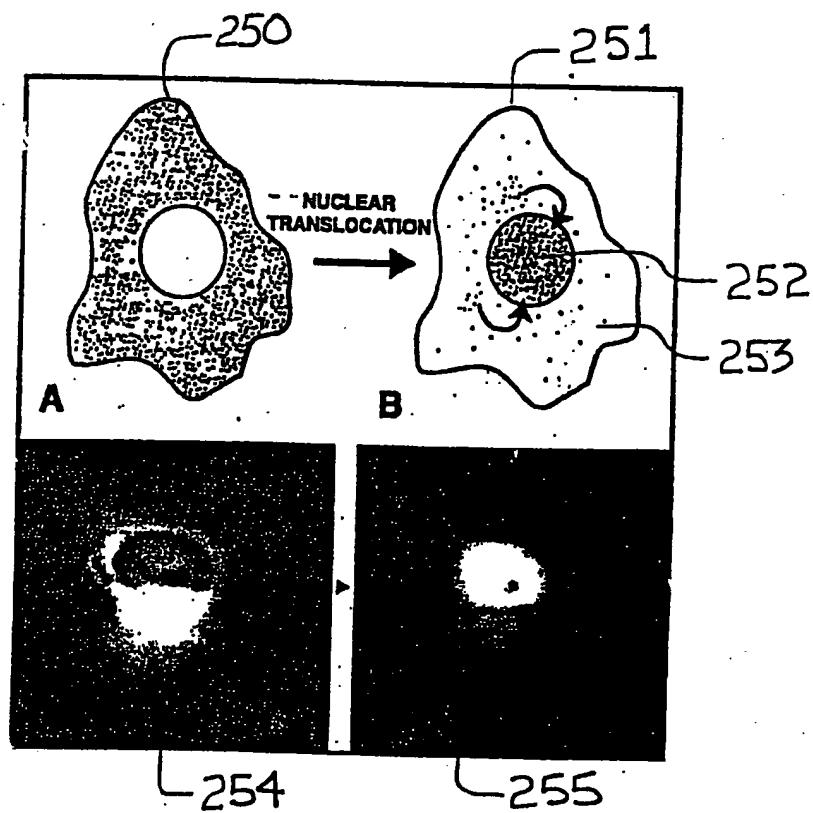


FIGURE 20

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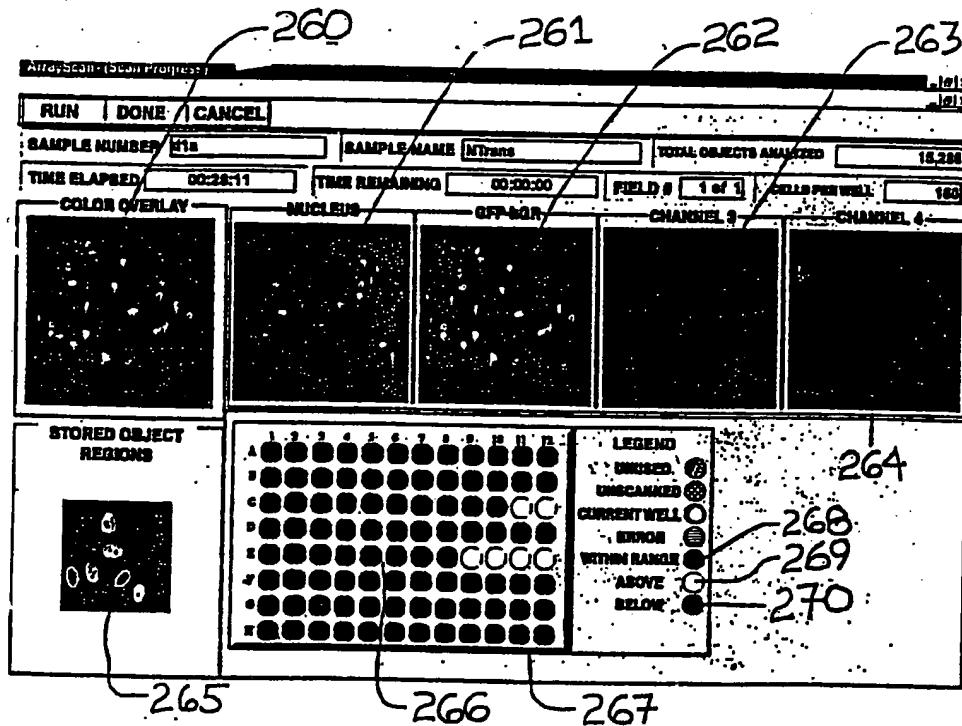
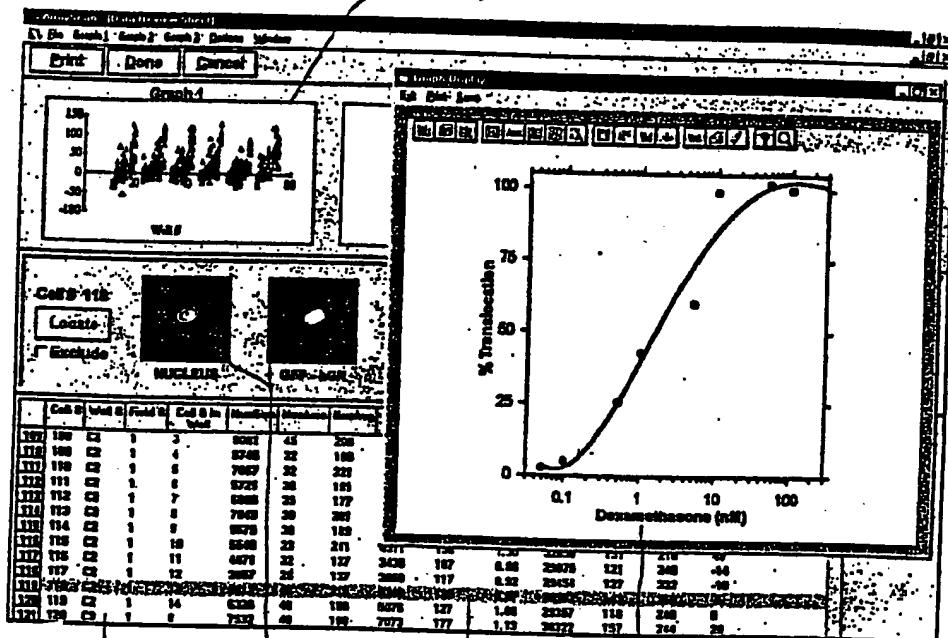


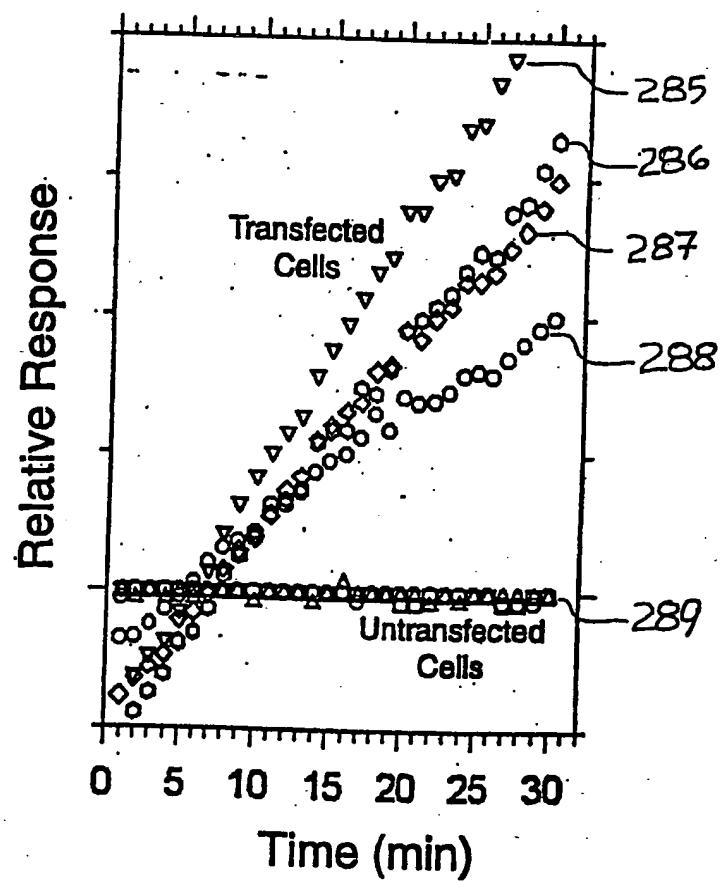
FIGURE 21

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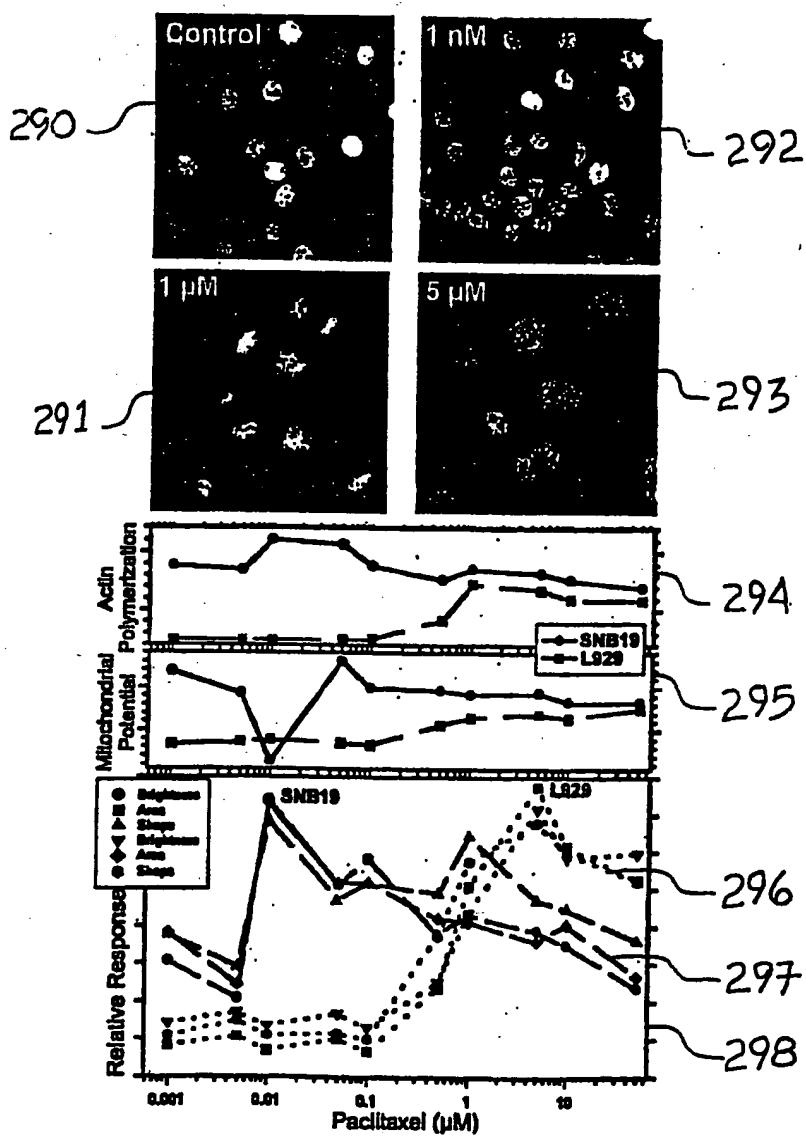


FIGURE 24

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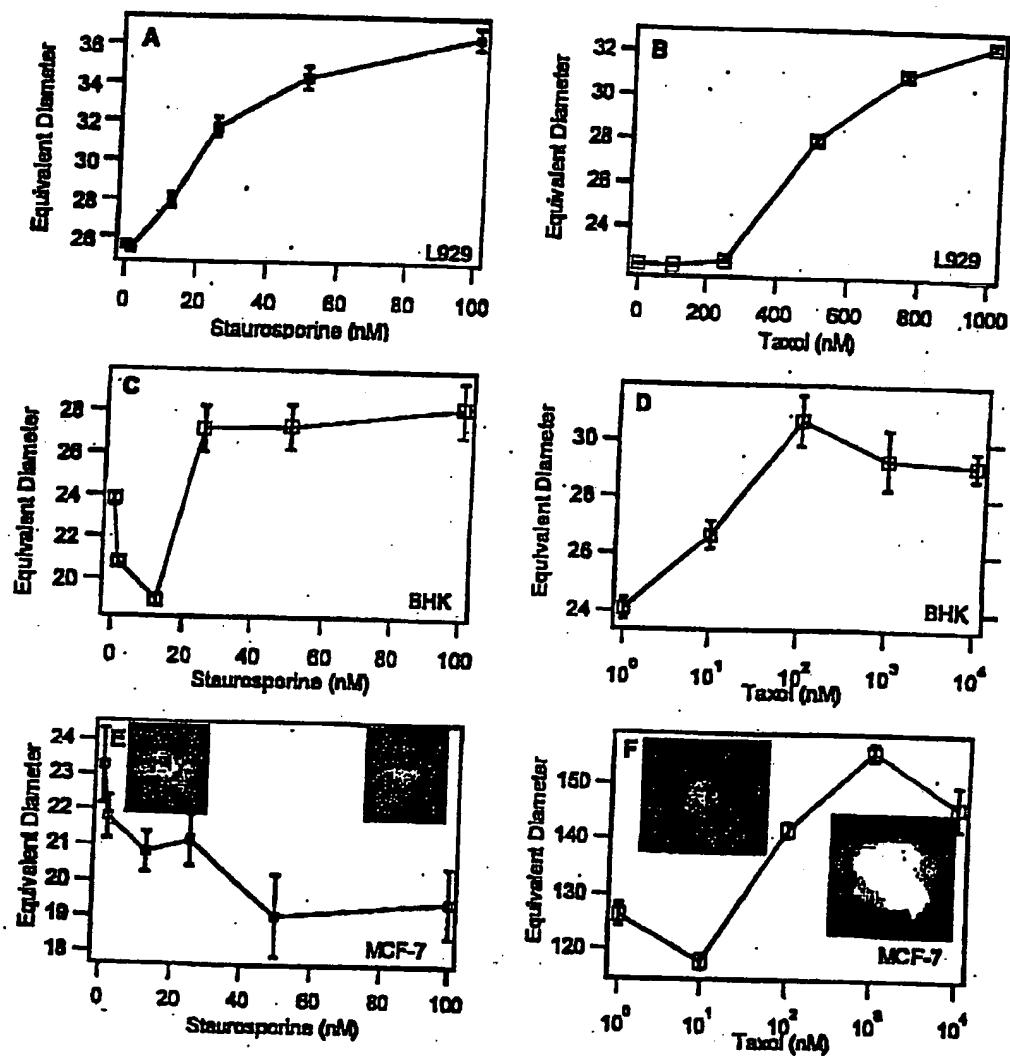
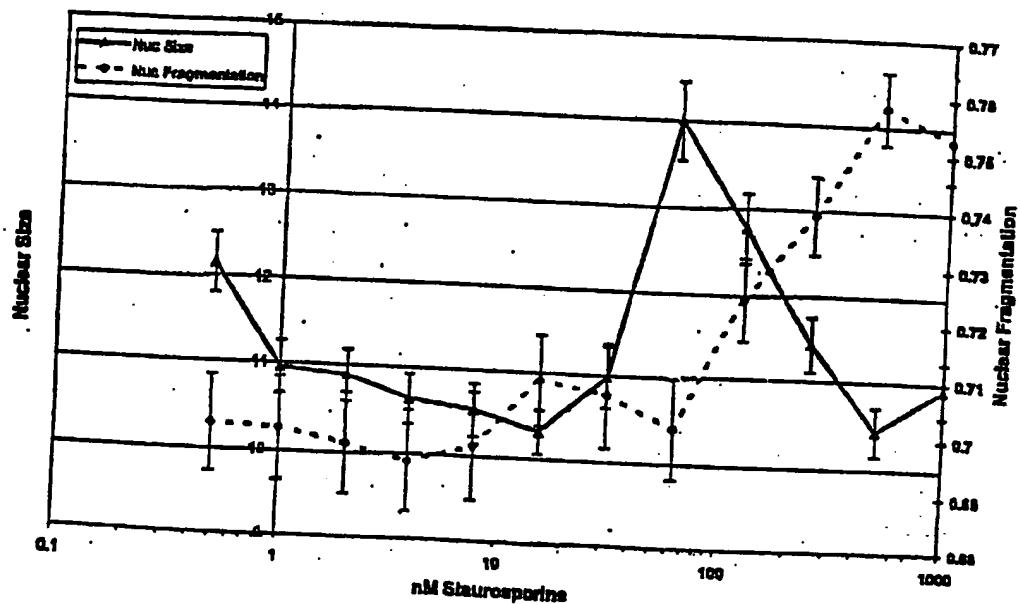


FIGURE 25

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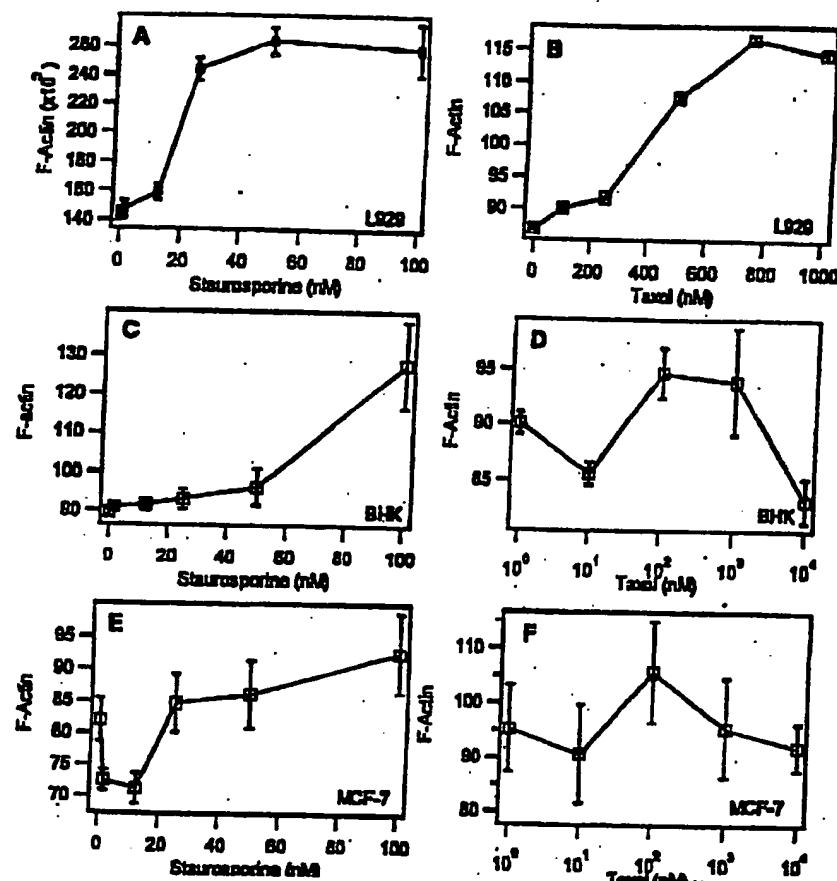
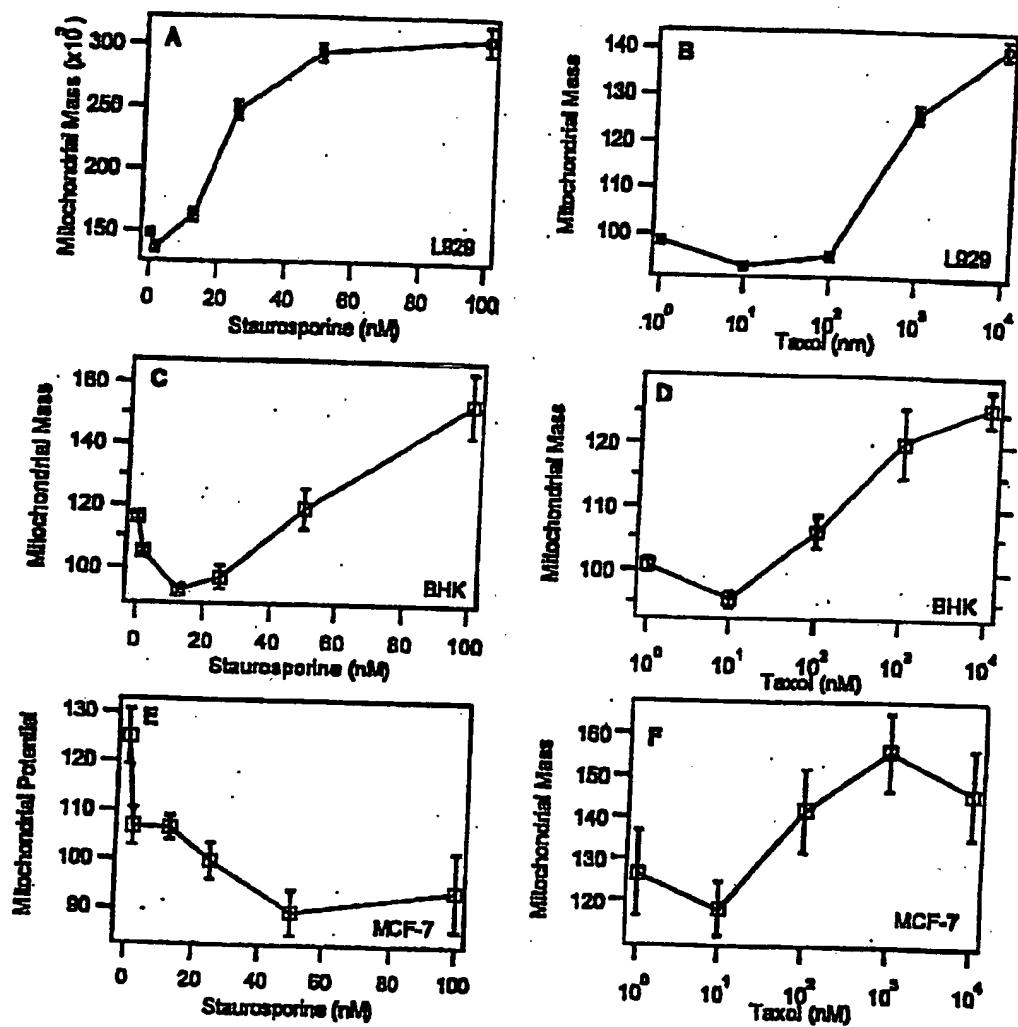


FIGURE 27

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**FIGURE 28**

Mitochondrial Mass, Potential Data

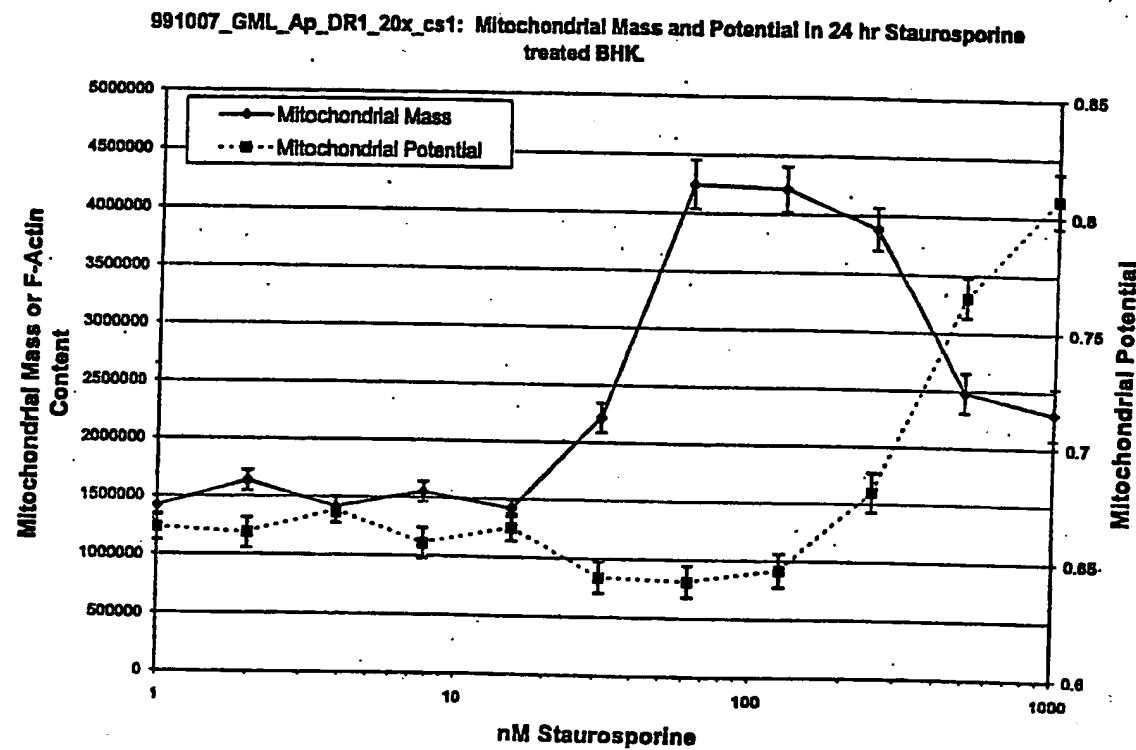


FIGURE 28G

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1. SIGNAL SEQUENCES

EPITOPE	SEQUENCE	SEQ ID NO.	REFERENCE
FLAG epitope	5' GACTACAAAGACGACG AA Seq: ACGACAAA	35 36	Kasir, et al., 1999. J Biol Chem. 274:24873-80.
HA epitope	5' TACCCATACGACGTACCAAGACTACGCA AA Seq: YPYDVPDYA	37 38	Smith, et al., 1999. J Biol Chem. 274:18894-900.
KT3 epitope	5' CCACCAGAACAGAAACA AA seq: PPEPET	39 40	MacArthur and Walter. 1984. J Virol. 52:483-91.
Myc epitope	5' GCAGAAGAACAAAAATTATAAGCGAAGA AGACTTA AA Seq: AEEQKLISEEDL	41 42	Gosney, et al., 1990. Anticancer Res. 10:623-8.

EYFP: SEQ ID NO: 43 (Nucleic acid); SEQ ID NO:44 (Amino acid)

M V S K G E E L F T G V V P I L V E L D
 ATGGTGAGCAAG GGCGAGGAGCTG TTCACCGGGGTG GTGCCCATCCTG GTCGAGCTGGAC

G D V N G H K F S V S G E G E G D A T Y
 GGCGACGTAAAC GGCCACAAGTTC AGCGTGTCCGGC GAGGGCGAGGGC GATGCCACCTAC

G K L T L K F I C T T G K L P V P W P T
 GCGAAGCTGACC CTGAAGTTCATC TGCAACCACCGGC AAGCTGCCGTG CCCCTGGCCCACC

L V T T F G Y G L Q C F A R Y P D H M K
 CTCGTGACCACC TTGGGCTACGGC CTGCAGTGCTTC GCCCGCTACCCC GACCACATGAAG

Q H D F F K S A M P E G Y V Q E R T I F
 CAGCACGACTTC TTCAAGTCCGCC ATGCCCGAAGGC TACGTCCAGGAG CGCACCATCTTC

F K D D G N Y K T R A E V K F E G D T L
 TTCAAGGACGAC GGCAACTACAAG ACCCGCGCCGAG GTGAAGTTCGAG GGCGACACCCCTG

V N R I E L K G I D F K E D G N I L G H
 GTGAACCGCATC GAGCTGAAGGGC ATCGACTTCAG GAGGACGGCAAC ATCCCTGGGGCAC

K L E Y N Y N S H N V Y I M A D K Q K N
 AAGCTGGAGTAC AACTACAACAGC CACAACGTCTAT ATCATGGCCGAC AAGCAGAAGAAC

G I K V N F K I R H N I E D G S V Q L A
 GGCATCAAGGTG AACTCAAGATC CGCCACAAATC GAGGACGGCAGC GTGCAGCTCGCC

D H Y Q Q N T P I G D G P V L L P D N H
 GACCACTACCAG CAGAACACCCCC ATCGGCGACGGC CCCGTGCTGCTG CCCGACAAACCAC

Y L S Y Q S A L S K D P N E K R D H M V
 TACCTGAGCTAC CAGTCCGCCCTG AGCAAAGACCCC AACGAGAAGCGC GATCACATGGTC

L L E F V T A A G I T L G M D E L Y K
 CTGCTGGAGTTC GTGACCGCCGCC GGGATCACTCTC GGATGGACGAG CTGTACAAG

EGFP: SEQ ID NO:45 (Nucleic acid); SEQ ID NO:46 (Amino acid)

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G D V N G H K F S V S G E G E G D A T Y
 GGCGACGTAAAC GGCCACAAGTTC AGCGTGTCCGGC GAGGGCGAGGAC GATGCCACCTAC

G K L T L K F I C T T G K L P V P W P T
 GGCAAGCTGACC CTGAAGTTCATC TGCAACCACGGC AAGCTGCCGTG CCCCTGGCCCCACC

L V T T L T Y G V Q C F S R Y P D H M K
 CTCGTGACCACC CTGACCTACGGC GTGCAGTGCCTTC AGCGCTACCC GACCACATGAAG

Q H D F F K S A M P E G Y V Q E R T I F
 CAGCACGACTTC TTCAAGTCCGCC ATGCCGAAGGC TACGTCCAGGAG CGCACCATCTTC

F K D D G N Y K T R A E V K F E G D T L
 TTCAAGGACGAC GGCAACTACAAG ACCCGCGCCGAG GTGAAGTTCGAG GGCGACACCCCTG

V N R I E L K G I D F K E D G N I L G H
 GTGAACCGCATC GAGCTGAAGGGC ATCGACTTCAAG GAGGACGGCAC ACCTGGGGCAC

K L E Y N Y N S H N V Y I M A D K Q K N
 AAGCTGGAGTAC AACTACAACAGC CACAACGTCTAT ATCATGGCCGAC AAGCAGAAGAAC

G I K V N F K I R H N I E D G S V Q L A
 GGCACTCAAGGTG AACTCAAGATC CGCCACAAACATC GAGGACGGCAGC GTGCAGCTGCC

D H Y Q Q N T P I G D G P V L L P D N H
 GACCACTACCAAG CAGAACACCCCC ATCGCGACGGC CCCGTGCTGCTG CCCGACAAACAC

Y L S T Q S A L S K D P N E K R D H M V
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L L E F V T A A G I T L G M D E L Y K
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EBFP: SEQ ID NO:47 (Nucleic acid); SEQ ID NO:48 (Amino acid)

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G D V N G H K F S V S G E G E G D A T Y
 GGCGACGTAAAC GGCCACAAGTTC AGCGTGTCCGGC GAGGGCGAGGGC GATGCCACCTAC
 G K L T L K F I C T T G K L P V P W P T
 GGCAAGCTGACC CTGAAGTTCATC TGACCCACCGGC AAGCTGCCGTG CCCTGGCCCCACC
 L V T T L T H G V Q C F S R Y P D H M K
 CTCGTGACCACC CTGACCCACCGGC GTGCAGTGTTC AGCCGCTACCCC GACCACATGAAG
 Q H D F F K S A M P E G Y V Q E R T I F
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 F K D D G N Y K T R A E V K P E G D T L
 TTCAAGGACGAC GGCAACTACAAG ACCCGCGCCGAG GTGAAGTTCGAG GGCGACACCCCTG
 V N R I E L K G I D F K E D G N I L G H
 GTGAACCGCATH GAGCTGAAGGGC ATCGACTCAAG GAGGACGGCAAC ATCCCTGGGGCAC
 K L E Y N F N S H N V Y I M A D K Q K N
 AAGCTGGAGTAC AACTTCAACAGC CACAACGTCTAT ATCATGGCCGAC AAGCAGAAGAAC
 G I K V N F K I R H N I E D G S V Q L A
 GGCACTCAAGGTG AACTTCAAGATC CGCCACAAACATC GAGGACGGCAGC GTGCAGCTGCC
 D H Y Q Q N T P I G D G P V L L P D N H
 GACCACTACCCAG CAGAACACCCCC ATCGGCACGGC CCCGTGCTGCTG CCCGACAACAC
 Y L S T Q S A L S K D P N E K R D H M V
 TACCTGAGCACC CAGTCCGCCCTG AGCAAAGACCCC AACGAGAAGCGC GATCACATGGTC
 L L E F V T A A G I T L G M D E L Y K
 CTGCTGGAGTTC GTGACCGCCGCC GGGATCACTCTC GGCATGGACGAG CTGTACAAG

ECFP: SEQ ID NO:49 (Nucleic acid); SEQ ID NO:50 (Amino acid)

M V S K G E E L F T G V V P I L V E L D
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 G D V N G H K F S V S G E G E G D A T Y
 GGCGACGTAAAC GGCCACAAGTTC AGCGTGTCCGGC GAGGGCGAGGGC GATGCCACCTAC
 G K L T L K F I C T T G K L P V P W P T
 GGCAAGCTGACC CTGAAGTTCATC TGACCCACCGGC AAGCTGCCGTG CCCTGGCCCCACC
 L V T T L T W G V Q C F S R Y P D H M K
 CTCGTGACCACC CTGACCTGGGGC GTGCAGTGTTC AGCCGCTACCCC GACCACATGAAG
 Q H D F F K S A M P E G Y V Q E R T I F
 CAGCACGACTTC TTCAAGTCCGCC ATGCCGAAGGC TACGTCCAGGAG CGCACCATCTTC

F K D D G N Y K T R A E V K F E G D T L
 TTCAAGGACGAC GGCAACTACAAG ACCCGCGCCGAG GTGAAGTCGAG GGGACACCCCTG
 V N R I E L K G I D F K E D G N I L G H
 GTGAACCCCATC GAGCTGAAGGGC ATCGACTTCAAG GAGGACGGCAAC ATCCCTGGGCAC
 K L E Y N Y I S H N V Y I T A D K Q K N
 AAGCTGGAGTAC AACTACATCAGC CACAACGTCTAT ATCACCGCCGAC AAGCAGAAGAAC
 G I K A N F K I R H N I E D G S V Q L A
 GGCATCAAGGCC AACTTCAAGATC CGCCACAACATC GAGGACGGCAGC GTGCAGCTCGCC
 D H Y Q Q N T P I G D G P V L L P D N H
 GACCACTACCAAG CAGAACACCCCCC ATCGGGCACGGC CCCGTGCTGCTG CCCGACAAACAC
 Y L S T Q S A L S K D P N E K R D H M V
 TACCTGAGCACC CAGTCCGCCCTG AGCAAAGACCCC AACGAGAAGCGC GATCACATGGTC
 L L E F V T A A G I T L G M D E L Y K
 CTGCTGGAGTTC GTGACCGCCGCC GGGATCACTCTC GGCATGGACGAG CTGTACAAG

Fred25: SEQ ID NO:51 (Nucleic acid); SEQ ID NO:52 (Amino acid)

M A S K G E E L F T G V V P I L V E L D
 ATGGCTAGCAAA GGAGAAGAACTC TTCAGGGAGTT GTCCAATTCTT GTGAATTAGAT
 G D V N G H K F S V S G E G E G D A T Y
 GGTGATGTTAAC GGCCACAAGTTC TCTGTCAGTGA GAGGGTGAAGGT GATGCAACATAC
 G K L T L K F I C T T G X L P V P W P T
 GGAAAACCTTACCT CTGAAGTTCATC TGCACTACTGGC AAACTGCTGTT CCATGGCCAACA
 L V T T L C Y G V Q C F S R Y P D H M K
 CTAGTCACTACT CTGTGCTATGGT GTTCAATGCTTT TCAAGATAACCG GATCATATGAAA
 R H D F F K S A M P E G Y V Q E R T I F
 CGGCATGACTTT TTCAAGAGTGCC ATGCCGAAGGT TATGTACAGGAA AGGACCATCTTC
 F K D D G N Y K T R A E V K F E G D T L
 TTCAAAGATGAC GGCAACTACAAG ACACGTGCTGAA GTCAAGTTGAA GGTGATACCCCTT
 V N R I E L K G I D F K E D G N I L G H
 GTTAATAGAACATC GAGTTAAAGGT ATTGACTTCAAG GAAGATGGCAAC ATTCTGGACAC
 K L E Y N Y N S H N V Y I M A D K Q K N
 AAATTGGAATAC AACTATAACTCA CACAATGTATAC ATCATGGCAGAC AAACAAAAGAAT
 G I K V N F K T R H N I E D G S V Q L A
 GGAATCAAAGTG AACTTCAAGACC CGCCACAACATT GAAGATGGAAGC GTTCAACTAGCA
 D H Y Q Q N T P I G D G P V L L P D N H

GACCATTATCAA CAAAATACTCCA ATTGGCGATGGC CCTGTCCCTTTA CCAGACAACCAT

Y L S T Q S A L S K D P N E K R D H M V
TACCTGTCCACA CAATCTGCCCTT TCGAAAGATCCC AACGAAAAGAGA GACCACATGGTC

L L E F V T A A G I T H G M D E L Y N *
CTTCTTGAGTTT GTAACAGCTGCT GGGATTACACAT GGCATGGATGAA CTGTACAACTAG

2. PROTEASE RECOGNITION SITES

Substrate Recognition Sequences	Source	Recognition Site	SEQ ID NO	Reference
Caspase-1,4,5	peptide library	5'(TGG,TTA)GAACATGACAA Seq:(W,L)EHDV	53 54	Thornberry et al., 1997, J. Biol. Chem. 272:17907
proCaspase-1	peptide library	5'TGGTTAAAGAC AA Seq: WFKD/	55 56	Thornberry et al., 1997, J. Biol. Chem. 272:17907
Caspase-2	peptide library	5'GACGAACACGAC AA Seq: DEHD/	57 58	Thornberry et al., 1997, J. Biol. Chem. 272:17907
Caspase 3, 7	PARP	5'GACGAAGTTGAC AA Seq: DEVD/	59 60	Beneke, et al., 1997, Biochem Mol Biol Int. 43:755-61; Thornberry et al., 1997, J. Biol. Chem. 272:17907
ProCaspase 3	Caspase-3	5'ATAGAAACAGAC AA Seq: IETD/	61 62	Tewari, M., et al., 1995, Cell. 81:801-9.
ProCaspase-4,5	peptide library	5'TGGCTAACAGAC AA Seq: WVRD/	63 64	Thornberry, N.A. et al., 1997, J.Biol. Chem. 272, 17907-17911
Caspase 6	Lamin A, peptide library	5'GTAGAAATAGAC AA Seq: VEID/ 5'GTAGAACACGAC AA Seq: VEHD/	65 66 67 68	Nakajima and Sado. 1993. Biochim Biophys Acta. 1171:311-4; Thornberry et al., 1997, J. Biol. Chem. 272:17907
proCaspase 6	Caspase-6	5'ACAGAAAGTAGAC AA Seq: TEVD/	69 70	Fernandes-Alnemri, et al., 1994, J. Biol. Chem. 269:30761-4.
proCaspase-7	peptide library	5'ATACAAGCAGAC AA Seq: IQAD/	71 72	Thornberry, N.A. et al., 1997, J.Biol. Chem. 272, 17907-17911
Caspase 8	peptide library	5'GTAGAAACAGAC AA Seq: VETD/	73 74	Muzio, M., et al., 1996, Cell. 85:817-27; Fernandes-Alnemri, et al., 1996, Proc Natl Acad Sci U S A. 93:7464-9; Thornberry et al., 1997, J. Biol. Chem. 272:17907
proCaspase-8	Caspase-8	5'TTAGAAACAGAC AA Seq: LETD/	75 76	Muzio, M., et al., 1996, Cell. 85:817-27; Fernandes-Alnemri, et al., 1996, Proc Natl Acad Sci U S A. 93:7464-9; Thornberry et al., 1997, J. Biol. Chem. 272:17907
Caspase 9	peptide library	5'TTAGAACACGAC AA Seq: LEHDV/	77 78	Thornberry, N.A. et al., 1997, J.Biol. Chem. 272, 17907-17911
proCaspase 9	Caspase-9	CCCGAAACCCGAC PEPD	79 80	Thornberry, N.A. et al., 1997, J.Biol. Chem. 272, 17907-17911
HIV protease		5'AGCCAAAATTAC AA Seq: SQNY/ 5'CCAAATAGTACAA AA Seq: PIVQ/	81 82 83 84	Matayoshi, et al., 1990, Science, 247:954-8.
Adenovirus endopeptidase		5'AUOTTGGAGGA AA Seq: MFGG/ 5'GCAAAAAAAAAGA AA Seq: AKKR/	85 86 87 88	Weber and Tihanyi. 1994, Methods Enzymol. 244:595-604.
b-Secretase	Amyloid precursor protein	5'GTAAAAAUG AA Seq: VKM/ 5'QACGCAGAATTTC DAEF/	89 90 91 92	Hardy et al., 1994, in Amyloid Protein Precursor in Development, Aging, and Alzheimer's Disease, ed. C.L. Masters et al., pp. 190-198.
Cathepsin D		5'AAACCAGCATTATTTC AA Seq: KPALF 5'TTCAGATTA AA Seq: FRL/	93 94 95 96	Dunn, et al., 1998, Adv Exp Med Biol. 436:133-8.
Matrix Metalloproteases		5'GGACCATTAGGACCA AA Seq: GPLOP	97 98	Bouvier et al., 1993; Garbett et al., 1999; Hill and Sakanari, 1997;

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				Kojima et al., 1998; Tyagi et al., 1995; Wilhelm et al., 1993; Williams and Auld, 1986; Haugland, R., Handbook of fluorescent probes and research Chemicals 7th ed.
Granzyme B	peptide library	5'ATAGAACCCAGAC AA Seq: IEPDN	99 100	Thomberry et al., 1997, J. Biol. Chem. 272:17907
Anthrax protease	MEK1	5'ATGCCCAAGAAGAAGCCGAC GCCCATCCAGCTGAACCC AA Seq: MPKKKPTPIQLN	101 102	Vitale et al., (1998) Biochem Biophys Res Commun 248 (3), 706-711
Anthrax protease	MEK2	5'ATGCTGGCCCGGAGGAAGCCG GTGCTGCCGGCGCTACCATCA ACCC AA Seq: MLARRKPVLPAUTIN	103	Vitale et al., (1998) Biochem Biophys Res Commun 248 (3), 706-711
tetanus/botulinum	cellubrevin	5'GCCTCGCAAGTTGAAACA AA Seq: ASQFET	104 105 106	McMahon et al., Nature 364:346-349; Martin et al., J. Cell Biol. In press
tetanus/botulinum	synaptobrevin/ VAMP3	5'GCTTCTCAATTGAAACG AA Seq: ASQFET	107 108	Schiavo et al., (1992) Nature 359, 832-5
Botulinum neurotoxin A	SNAP-25	5'GCCAACCAACGTGCAACA AA Seq: ANQ/RAT	109 110	Zhao, et al. Gene 145 (2), 313-314 (1994)
Botulinum neurotoxin B	VAMP	5'GCTTCTCAATTGAAACG AA Seq: ASQ/FET	111 112	
Botulinum neurotoxin C	Syntaxin	5'ACGAAAAAAAGCTGTGAAA AA Seq: TKK/AVK	113 114	Martin et al., J. Leukoc. Biol. 65 (3), 397-406 (1999)
Botulinum neurotoxin D	VAMP	5'GACCAGAAGCTCTGAG AA Seq: DQK/LSE	115 116	
Botulinum neurotoxin E	SNAP-25	5'ATCGACAGGATCATGGAG AA Seq: IDR/IME	117 118	
Botulinum neurotoxin F	VAMP	5'AGAGACCAAGAAGCTCTCT AA Seq: RDQ/KLS	119 120	
Botulinum neurotoxin G	VAMP	5'ACGAGCGCACCCAAGTTG AA Seq: TSA/AKL	121 122	

3. PRODUCT/REACTANT TARGET SEQUENCES

Target	Target Source	Target domain (Product or Reactant)	SEQ ID NO	Reference
Cytoplasm/cytoskeleton	Annexin II	5'ATGTCTACTGTCCACGAAATCTGTCAAGCTCAGCTGGAGGGTGTTCATTCTACACCCCCAACGTGCC 3' (Amino acid seq: M S T V H E I L C K L S L E G V H S T P P S A)	123 124	Eberhard, et al., 1997, Mol. Biol. Cell 8:293a.
Inner surface of plasma membrane	farnesylation	5'AUGGGATCTACATTAAGCGCAGAACAAAGCAGCACTAGAAAAGAAGCAAAUGATAGACAGAACTTTAAAGAGAAAGACGGAGAAAAAGCTGCTAGA 3' (AA seq: M Q C T L S A E D K A A V E R S K M I D R N L R E D G E K A A R)	125 126	Ferruccio G, et al., J. Biol. Chem. 274, 5843-5850, 1999
Nucleus	NFkB p50	5'AGAAGGAAACGACAAAAG (AA seq: R R K R Q K)	127 128	Henkel, T et al., Cell 68, 1121-1133, 1992
Nucleolus	NOLP	5'AGAAAACGTATACTGACTTACCTCAAGTCC TGCAGGGGGATGAAAAGAAGTGTTTTGAGATGTCTCACCTTACCTCCACCTTACT (AA seq: R K R I R T Y L K S C R R M K R S G F E M S R P I P S H L T)	129 130	Ueki, et al., 1998. Biochem Biophys Res Commun. 252:97-102.
Mitochondria	cytochrome c oxidase	5'ATGTOCCGCTCTGACGCCCTGCTGCTGGGG GCCTTGACAGGTCTGGCCCGGGCTCCAG TGCGCGCCCAAGATCCATTCGTTG (AA Seq: M S V L T P L L R Q L T O S A R R L P V P R A L I H S L)	131 132	Rizzuto, et al., 1989. J Biol Chem. 264:10595-600.
Nuclear Envelope	ODV-E66 & ODV-E25	5'AUGAGCATTTATAAAATTGTTATTGGA TTTTTATAATATGTTTTTATATTTAACAA (AA Seq: M S I V L I I V V I F L I C F L Y L S N S K D P R V P V E L M)	133 134	Hong, T, et al. PNAS, 94, 4050-4055, 1997
Colgi	Calreticulin	5'ATGAGGCTTCGGGAGCCGCTCCGTAGCGGC AGCGCCGCGATGCCAGGCGCGTCCCTACAGC GGGCGCTGCGCCTGCTCGTGGCCGTCTGCGCT CTGCACTTGGCGTCACCCCTGTTACTACCT GCGTGGCGGAGCTGAGCCGCTGCCCCAA CTGCTGGAGCTCCACACCGCTGAGGGCG GCTCGAACAGTGCCGCCGCGCATGGGCAGTC CTCCGGGGAGCTCCGGACCGAGGGGCC (AA Seq: M R L R E P L L S G S A A M P Q A S L Q R A C R L L V A V C A L H L G V T L V Y Y L A G R D L S R L P Q L V G V S T P L Q Q G S N S A A A I G Q S S G E L R T G G A)	135 136	Fliegel, L., et al., J. Biol. Chem. 264, 21522-21528, 1989.
Endoplasmic reticulum	D-AKAP1	5'GAAACAATAAGACCTATAAGAAGATGAGT ACATITACATCTACAGACAGCAAAAUUGCACAA TICAATTAAGATCTCCCTTCCATTAGCATTA CCAGGAAUGTAGCTTATTAGGATGGTGGT GGTTCCTCAGTAGAAAAAAA (AA Seq: E T I R P I R I R R C S Y F T S T D S K M A I Q L R S P F P L A L P Q M L A L L G W W W F F S R K K)	137 138	Huang, L.J. Et al., J. Cell. Biol. 145, 951-959, 1999
Nuclear Export	MEK1	5'GCCTTGCGAGAAGAGCTGGAGGAGCT AGAGCTTGATGAG	139	Fukuda, (1997) J. Biol. Chem

FIGURE 29C

		(AA SEQ: A L Q K K L E E L E L D E	140	272, 51, 32642- 32648
Size exclusion	PROJ domain of MAP4	S'GCCGACCTCACTCTTGTGGATGCGTGACCA GAACCACCTTCAGAAAATTGAGGGAGAAATAA AGCGAGACTTCATGGCTGGCTGGAGGCAGA GCCCTATGATGACATCGTGGGAGAAACTGTG GAGAAAAACTGAGTTTATTCCTCTCCCTGGATGG TGATGAGAAAACCCGGAAACTCAGAGTCCAAA AAGAAAACCCCTGCTTAGACACTAGCCAGGGTGA AAGGTATCCCATCTCTAAACCAACACTCTTA GCCAATGGTGATCATGGAAATGGAGGGGAAATA ACACTGGCAGGGCTCCAACTGACTCTCTTGA GAGAGAGTGGACTATCCGGATTATCAGACCA GCLAGAACTGGCAGAAGATGCAAGCTTTG TTTCAGCCCTCAAGCAAGTGTAGATACTGACC AGGCTOAGCCCTTAAACGAGCACCGTGATGAA TGGTTGGCAGATCTGCTCTTGTCTCCAGTG GACCCACGAACGCTTCATGCACTTACAGAGCG AGACAATCTTCAGAAAGACAGTTACGGTATG CTTCCCTGTGACTCATTTGCTTCCACGGCTGT TGATCTCAGGAGTGGCTGTGGGAGCCCCA AACTCTCATGTCAGAGTCTGTGTCTTCCC AGAGGTTACTATAGAAACCCATACAGCAGCA ACAGAGCTCTCAAGGCAGCAGAAGTGGAA CAGTQAAGAGCAGCTGCCAGCTAAAGCATT GGAACAGATGGCAGAGCAGACACTQATGTG GTGCACTCTCCATCCACAGACACAACACCAAG GCCAGACACAGAGGCAGCAGTGGCTAAAGA CATAGAAGAGATCACCAAGCCAGATGATA TTGGCAAATGTCAGCGAGCCATCTACTGAAT CGGATATGTTCTGGCCAGGACATGGAAC ACTCACAGGAACAGAGGCAGGCCACGCTAAC AATATCATATTGCTTACAGAACAGACGAAAT CTICAACCAAGGATGTAGCACCCACCTATGGA AGAAGAAAATTGTCAGGCAATGATA	141	West, (1991). J Biol Chem 266(32): 21886- 96; Olson, K. R. (1995). J Cell Biol 130(3): 639- 50.
		(AA SEQ: A D L S L V D A L T E P P P E I E G E I K R D F M A A L E A E P Y D D I V G E T V B K T E F I P L L D G D E K T G N S E S K K K P C L D T S Q V E G I P S S K P T L L A N G D H G M E G N N T A G S P T D F L E E R V D Y P D Y Q S S Q N W P E D A S F C F Q P Q Q V L D T D Q A E P F N E H R D D G L A D I L F V S S G P T N A S A F T E R D N P S E D S Y G M L P C D S F A S T A V V S Q E W S V G A P N S P C S E S C V S P E V T I E T L Q P A T E L S K A A E V E S V K E Q L P A K A L E T M A E Q T T D V V H S P S T D T T P G P D T E A A L A K D I E E I T K P D V I L A N V T Q P S T E S D M F L A Q D M E L L T G T B A A H A N N I I L P T E P D E S S T K D V A P P M E E E I V P G N D T T S P K E T E T T L P I K M D L A P P E D V L L T K E T E L A P A K G M V S L S E I E A L A K N D V R S A E I P V A Q E T V V S E T E V V L A T E V V L P S D P I T T L T K D V T L P L E A E R P L V T D M T P S L E T E M T L G K E T A P P T E T N L G M A K D M S P L P E S E V T L G K D V V I L P E T K V A E F N N V T P L S E E E V T S V K D M S P S A E T E A P L A K N A D L H S G T E L I V D N S M A P A S D L A L P L E T K V A T V P I K D K G	142	
Vesicle membrane	Synaptobrevin	5'ATGTGGGCAATCGGGATTACTGTTCT GGTTATCTTCATCATCATCATCATCATCGTG TGGGGTGTGTC (AA SEQ: M W A I G I T V L V I F I I I I I V W V V)	143	Schlavo et al., (1992) Nature 359, 832-5
			144	

Vesicle membrane	Cellubrevin	5' ATGTGGCGATAGGGATCAGTGTCC GGTGATCATTGTCAATCATCATCATCGTG TGGTGTG (AA SEQ: M W A I G I S V L V I I V I I I I V W C)	145 146	McMahon et al., Nature 364:346- 349; Martin et al., J. Cell Biol. In press
Nuclear Export	MEK2	5' GACCTGCAGAAGAACGCTGGAGGAGCT GGAACCTTGACGAG AA SEQ: DLQKKLEELDE	147 148	Zheng and Guan, J. Biol. Chem. 268:11435-11439, 1993
Peroxisome	PX	5' TCTAACTG AA SEQ: S K L	149 150	Amery et al., Biochem. J. 336:367-371 (1998)

Microtubules (MAP4) SEQ ID NO:151 (Nucleic acid); SEQ ID NO:152 (amino acid)

MAP4:

M A D L S L V D A L T E P P P E I E G E
ATGGCCGACCTC AGTCTTGTGGAT GCGTTGACAGAA CCACCTCCAGAA ATTGAGGGAGAA
TACCGGCTGGAG TCAGAACACCTA CGCAACTGTCTT GGTGGAGGTCTT TAACTCCCTCTT

I K R D F M A A L E A E P Y D D I V G E
ATAAAAGCGAGAC TTCATGGCTCGC CTGGAGGCAGAG CCCTATGATGAC ATCGTGGGAGAA
TATTCGCTCTG AAGTACCGACGC GACCTCCGCTC GGGATACTACTG TAGCACCCCTCTT

T V E K T E F I P L L D G D E K T G N S
ACTGTGGAGAAA ACTGAGTTTATT CCTCTCCTGGAT GGTGATGAGAAA ACCGGGAACCTCA
TGACACCTCTTT TGACTCAAATAA GGAGAGGACCTA CCACTACTCTT TGGCCCTTGAGT

E S K K K P C L D T S Q V E G I P S S K
GAGTCCAAAAAG AAACCTGCTTA GACACTAGCCAG GTTGAAGGTATC CCATCTCTAAA
CTCAGGTTTTTC TTTGGGACGAAT CTGTGATCGGTC CAACCTCCATAG GGTAGAAGATT

P T L L A N G D H G M E G N N T A G S P
CCAACACTCCTA GCCAATGGTGT CATGGAATGGAG GGGATAACACT GCAGGGTCTCCA
GGTTGTGAGGAT CGGTTACCACTA GTACCTTACCTC CCCTTATTGTGA CGTCCCAGAGGT

T D F L E E R V D Y P D Y Q S S Q N W P
ACTGACTTCCTT GAAGAGAGAGTG GACTATCGGAT TATCAGAGCAGC CAGAACTGGCCA
TGACTGAAGGAA CTTCTCTCTCAC CTGATAGGCCCTA ATAGTCTCGTCG GTCTTGACCGGT

E D A S F C F Q P Q Q V L D T D Q A E P
GAAGATGCAAGC TTTTGTGTCAG CCTCAGCAAGTG TTAGATACTGAC CAGGCTGAGCCC
CTTCTACGTTCG AAAACAAAGGTC GGAGTCGTTCAC AATCTATGACTG GTCCGACTCGGG

F N E H R D D G L A D L L F V S S G P T
TTAACGAGCAC CGTGATGATGGT TTGGCAGATCTG CTCTTGTCTCC AGTGGACCCACG
AAATTGCTCGTG GCACTACTACCA AACCGTCTAGAC GAGAACAGAGG TCACCTGGGTGC

N A S A F T E R D N P S E D S Y G M L P
AACGCTCTGCA TTTACAGAGCGA GACAATCCTCA GAAGACAGTTAC GGTATGCTTCCC
TTGCGAAGACGT AAATGTCTCGCT CTGTTAGGAAGT CTTCTGTCAATG CCATACGAAGGG

C D S F A S T A V V S Q E W S V G A P N
TGTGACTCATTT GCTTCCACGGCT GTTGTATCTAG GAGTGGTCTGTG GGAGCCCCAAAC
ACACTGAGTAAA CGAAGGTGCCGA CAACATAGAGTC CTCACCAGACAC CCTCGGGGTTTG

S P C S E S C V S P E V T I E T L Q P A
TCTCCATGTTCA GAGTCCCTGTGTC TCCCCAGAGGTT ACTATAGAAACC CTACAGCCAGCA
AGAGGTACAAGT CTCAGGACACAG AGGGGTCTCCA TGATATCTTGG GATGTCGGTCGT

T E L S K A A E V E S V K E Q L P A K A
ACAGAGCTCTCC AAGGCAGCAGAA GTGGAATCAGTG AAAGAGCAGCTG CCAGCTAAAGCA
TGTCTCGAGAGG TTCCGTCGTCTT CACCTTAGTCAC TTTCTCGTCGAC GGTCGATTTCGT

L E T M A E Q T T D V V H S P S T D T T
TTGGAAACGATG GCAGAGCAGACC ACTGATGTGGTG CACTCTCCATCC ACAGACACAACA
AACCTTGCTAC CGTCTCGTCTGG TGACTACACCAC GTGAGAGGTAGG TGTCTGTGTTGT

P G P D T E A A L A K D I E E I T K P D
CCAGGCCAGAC ACAGAGGCAGCA CTGGCTAAAGAC ATAGAAGAGATC ACCAAGCCAGAT
GGTCCGGTCTG TGTCTCCGTCGT GACCGATTCTG TATCTCTCTAG TGGTCGGTCTA

V I L A N V T Q P S T E S D M F L A Q D
GTGATATTGGCA AATGTCACGCAG CCATCTACTGAA TCGGATATGTTC CTGGCCAGGAC
CACTATAACCGT TTACAGTGCCTC GGTAGATGACTT AGCCTATACAAG GACCGGGTCTG

M E L L T G T E A A H A N N I I L P T E
ATGGAACTACTC ACAGGAACAGAG GCAGCCCACGCT ACAATATCATA TTGCCTACAGAA
TACCTTGATGAG TGTCTTGTCTC CGTCGGGTGCA TTGTTATAGTAT AACGGATGTCTT

P D E S S T K D V A P P M E E E I V P G
CCAGACGAATCT TCAACCAAGGAT GTAGCACCACCT ATGGAAGAAGAA ATTGTCCAGGC
GGTCTGCTTAGA AGTTGGTCTTA CATCGGGTGGAA TACCTCTCTT TAACAGGGTCCG

N D T T S P K E T E T T L P I K M D L A
AATGATACGACA TCCCCCAAAGAA ACAGAGACAACA CTTCCAATAAAA ATGGACTTGGCA
TTACTATGCTGT AGGGGGTTCTT TGTCTCTGTGT GAAGGTTATTTT TACCTGAACCGT

P P E D V L L T K E T E L A P A K G M V
CCACCTGAGGAT GTGTTACTTACCAAGAAACAGAA CTAGCCCCAGCC AAGGGCATGGTT
GGTGGACTCTCA CACAATGAATGG TTCTCTCTCTT GATCGGGTCCG TTCCCGTACCAA

S L S E I E R A L A K N D V R S A E I P
TCACTCTCAGAA ATAGAAGAGGCT CTGGCAAAGAAT GATGTCGCTCT GCAGAAATACCT
AGTGAGAGTCTT TATCTCTCCGA GACCGTTCTTA CTACAAAGCGAGA CGTCTTATGGA

V A Q E T V V S E T E V V L A T E V V L
GTGGCTCAGGAG ACAGTGGTCTCA GAAACAGAGGTG GTCTGGCAACA GAAGTGGTACTG
CACCGAGTCCTC TGTCACCAGAGT CTTGTCTCCAC CAGGACCGTTGT CTTCACCATGAC

P S D P I T T L T K D V T L P L E A E R
CCCTCAGATCCC ATAACAAACATTG ACAAAAGGATGTG ACACCTCCCTTA GAAGCAGAGAGA
GGGAGTCTAGGG TATTGTTGAAC TGTTCTACAC TGTGAGGGAAAT CTTCGTCTCTCT

P L V T D M T P S L E T E M T L G K E T
 CCGTTGGTGAACG GACATGACTCCA TCTCTGAAACA GAAATGACCCCA GGCAAAGAGACA
 GGCAACCACGTGC CTGTACTGAGGT AGAGACCTTGAT CTTTACTGGGAT CCGTTCTCTGT

A P P T E T N L G M A K D M S P L P E S
 GCTCCACCCACA GAAACAAATTG GGCATGGCCAAA GACATGTCCTCA CTCCCAGAATCA
 CGAGGTGGGTGT CTTGTTAAC CCGTACCGGTT CTGTACAGAGGT GAGGGTCTTAGT

E V T L G K D V V I L P E T K V A E F N
 GAAGTGACTCTG GGCAGGACGTG GTTATACTTCA GAAACAAAGGTG GCTGAGTTAAC
 CTTCACTGAGAC CCGTCCCTGCAC CAATATGAAGGT CTTGTTCCAC CGACTCAAATTG

N V T P L S E E V T S V K D M S P S A
 AATGTGACTCCA CTTCAGAAAGAA GAGGTAACCTCA GTCAAGGACATG TCTCCGTCTGCA
 TTACACTGAGGT GAAAGTCTCTT CTCCATTGGAGT CAGTTCTGTAC AGAGGCAGACGT

E T E A P L A K N A D L H S G T E L I V
 GAAACAGAGGCT CCCCTGGCTAAG AATGCTGATCTG CACTCAGGAACA GAGCTGATTGTG
 CTTTGTCTCCGA GGGGACCGATTC TTACGACTAGAC GTGAGTCCTGTGT CTCGACTAACAC

D N S M A P A S D L A L P L E T K V A T
 GACAACAGCATG GCTCCAGCCTCC GATCTTGCAC TG CCCTGGAAACA AAAGTAGCAACA
 CTGTTGTCGTAC CGAGGTGGAGG CTAGAACGTGAC GGGAACCTTGT TTTCATCGTTGT

V P I K D K G T V Q T E E K P R E D S Q
 GTTCCAATTAAA GACAAGGAACG GTACAGACTGAA GAAAAACCACGT GAAGACTCCCAG
 CAAGGTTAATTCT GTGTTCTTGA CATGTCTGACTT CTTTTGGTGC CTTCTGAGGGTC

L A S M Q H K G Q S T V P P C T A S P E
 TTAGCATCTATG CAGCACAAGGGA CAGTCAACAGTA CCTCCTTGCACG GCTTCACCAGAA
 AATCGTAGATAC GTCTGTTCCCT GTCACTTGTAC GGAGGAACGTGC CGAAGTGGTCTT

P V K A A E Q M S T L P I D A P S P L E
 CCAGTCAGGACT GCAGAACAAATG TCTACCTTACCA ATAGATGCACCT TCTCCATTAGAG
 GGTCTGTTCGA CGTCTGTTAC AGATGAAATGGT TATCTACGTGGA AGAGGTAATCTC

N L E Q K E T P G S Q P S E P C S G V S
 AACTTAGAGCAG AAGGAAACGCC GGCAGCCAGCCT TCTGAGCCTTGC TCAGGAGTATCC
 TTGAATCTCGTC TTCTTGCAGA CGCTCGGTGGGA AGACTCGAACG AGTCCTCATAGG

R Q E E A K A A V G V T G N D I T T P P
 CGGCAAGAAAGAA GCAAAGGCTGCT GTAGGTGTGACT GGAAATGACATC ACTACCCCGCCA
 GCGGTTCTCTT CGTTTCCGACGA CATCCACACTGA CCTTTACTGTAG TGATGGGGCGGT

N K E P P P S P E K K A K P L A T T Q P
 AACAAAGGAGCCA CCACCAAGCCC GAAAAGAAAGCA AAGCCTTGGCC ACCACTCAACCT
 TTGTTCTCGGT GGTGGTTGGGT CTTTCTTCTGT TTGGAAACCGG TGGTGAGTTGGA

A K T S T S K A K T Q P T S L P K Q P A
 GCAAAGACTTCA ACATCGAAAGCC AAAACACAGCCC ACTTCTCTCCCT AAGCAACCAGCT
 CGTTCTGAAAGT TGTAGCTTCCGG TTTTGTGTCGGG TCAAGAGAGGGGA TTGTTGGTGC

P T T S G G L N K K P M S L A S G S V P
 CCCACCA CCTCT GGTGGGTTGAAT AAAAACCCATG AGCCTCGCCCTCA GGCTCAGTGCCTA
 GGGTGGTGGAGA CCACCCA ACTTA TTTTTGGTAC TCGGAGCGGAGT CCGAGTCACCGT

A A P H K R P A A A T A T A R P S T L P
 GCTGCCACAC AAACGCCCTGCT GCTGCCACTGCT ACTGCCAGGCCT TCCACCCCTACCT
 CGACGGGGTGTG TTGCGGGACGA CGACGGTGACGA TGACGGTCCCGA AGGTGGGATGGA

A R D V K P K P I T E A K V A E K R T S
 GCCAGAGACGTG AAGCCAAAGCCA ATTACAGAAGCT AAGGTTGCCGAA AAGGGACCTCT
 CGGTCTCTCAC TTCGGTTCTGGT TAATGTCCTCGA TTCCAACGGCTT TTGCGCTGGAGA

P S K P S S A P A L K P G P K T T P T V
 CCATCCAAGCCT TCATCTGCCCA GCCCTCAAACCT GGACCTAAAACC ACCCCAAACCGTT
 GTAGGTTCGGA AGTAGACGGGGT CGGGAGTTGGA CCTGGATTGG TGGGTTGGCAA

S K A T S P S T L V S T G P S S R S P A
 TCAAAGCCACA TCTCCCTCAACT CTTGTTCCACT GGACCAAGTAGT AGAAGTCCAGCT
 AGTTTTCGGTGT AGAGGGAGTTGA GAACAAAGGTGA CCTGGTTCATCA TCTTCAGGTGCA

T T L P K R P T S I K T E G K P A D V K
 ACAACTCTGCCT AAGAGGCCAACC AGCATCAAGACT GAGGGGAAACCT GCTGATGTCAAA
 TGTGAGACCGA TTCTCCGGTTGG TCGTAGTTCTGA CTCCCCTTGGA CGACTACAGTT

R M T A K S A S A D L S R S K T T S A S
 AGGATGACTGCT AAGTCTGCCTCA GCTGACTTGAGT CGCTCAAAGACC ACCTCTGCCAGT
 TCCTACTGACGA TTCAGACGGAGT CGACTGAACTCA GCGAGTTCTGG TGGAGACGGTCA

S V K R N T T P T G A A P P A G M T S T
 TCTGTGAAGAGA AACACCACTCCC ACTGGGGCAGCA CCCCCCAGCAGGG ATGACTTCCACT
 AGACACTTCTCT TTGTTGGTGGAGG TGACCCCGTCGT GGGGGTCGTCCC TACTGAAGGTGA

R V K P M S A P S R S S G A L S V D K K
 CGAGTCAGGCC ATGTCCTGCACCT AGCCGCTCTTCT GGGGCTCTTCT GTGGACAAGAAC
 GCTCAGTTGGG TACAGACGTGGA TCGGCGAGAAGA CCCCCGAGAAAGA CACCTGTTCTC

P T S T K P S S S A P R V S R L A T T V
 CCCACTTCCACT AAGCCTAGCTCC TCTGCTCCAGG GTGAGCCGCTG GCCACAACGTT
 GGGTGAAGGTGA TTGGATCGAGG AGACGAGGGTCC CACTCGGCGGAC CGGTGTTGACAA

S A P D L K S V R S K V G S T E N I K H
 TCTGCCCCCTGAC CTGAAGAGTGTGTT CGCTCCAAGGTC GGCTCTACAGAA AACATCAAACAC
 AGACGGGGACTG GACTTCTCACAA GCGAGGTTCCAG CCGAGATGTCTT TTGTAGTTGTG

Q P G G G R A K V E K K T E A A T T A G
 CAGCCTGGAGGA GGCCGGCCAAA GTAGAGAAAAAA ACAGAGGCAGCT ACCACAGCTGG
 GTCGGACCTCTT CCGGCCCCGGTT CATCTTTTT TGTCTCCGTGCA TGGTGTGACCC

K P E P N A V T K A A G S . I A S A Q K P
 AAGCCTGAACCT AATGCAGTCACT AAAGCAGCCGGC TCCATTGCGAGT GCACAGAAACCG
 TTGGACTTGGGA TTACGTCACTGA TTTCGTGGCCG AGGTAACGCTCA CGTGTCTTGGC

P A G K V Q I V S K K V S Y S H I Q S K
 CCTGCTGGAAA GTCCAGATAGTA TCCAAAAAAGTG AGCTPAGTCAT ATTCAATCCAAG

GGACGACCCTTT CAGGTCTATCAT AGGTTTTTCAC TCGATGTCAGTA TAAGTTAGGTT
C V S K D N I K H V P G C G N V Q I Q N
TGTGTTCCAAG GACAATATTAAG CATGTCCTGGA TGTTGGCAATGTT CAGATTAGAAC
ACACAAAGGTT C TGTTATAATTC GTACAGGGACCT ACACCGTTACAA GTCTAAGTCITG
K K V D I S K V S S K C G S K A N I K H
AAGAAAAGTGGAC ATATCCAAGGTC TCCTCCAAGTGT GGGTCCAAGCT AATATCAAGCAC
TTCTTTCACCTG TATAGGTTCCAG AGGAGGTTTCACA CCCAGGTTTCGA TTATAGTTCGTG
K P G G G D V K I E S Q K L N F K E K A
AAGCCTGGTGGGA GGAGATGTCAAG ATTGAAAGTCAG AAGTTGAACTTC AAGGAGAAGGCC
TTCGGACCACCT CCTCTACAGTTC TAACTTTCACTG TTCAACTTGAAG TTCCCTCTCCGG
Q A K V G S L D N V G H F P A G G A V K
CAAGCCAAAGTG GGATCCCTTGAT AACGTTGGCCAC TTTCCTGCAGGA GGTGCCGTGAAG
GTTGGTTTCAC CCTAGGAACTA TTGCAACCGGTG AAAGGACGTCT CCACGGCACTTC
T E G G G S E A L P C P G P P A G E E P
ACTGAGGGCGGT GGCAGTGAGGCC CTTCCGTGTCCA GGCCCCCCCCTGGT GGGGAGGAGCCA
TGACTCCGCCA CGTCACTCCGG GAAGGCACAGGT CCGGGGGGGCGA CCCCTCTCGGT
V I P E A A P D R G A P T S A S G L S G
GTCATCCCTGAG GCTGCGCCTGAC CGTGGCGCCCT ACTTCAGCCAGT GGCCTCAGTGGC
CAGTAGGGACTC CGACGGGACTG GCACCGCGGGGA TGAAGTCGGTCA CCGGAGTCACCG
H T T L S G G G D Q R E P Q T L D S Q I
CACACCACCCCTG TCAGGGGGTGGT GACCAAAGGGAG CCCCAGACCTTG GACAGCCAGATC
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Q E T S I *
CAGGAGACAAGC ATCTAA
GTCCTCTGTTCG TAGATT

44/50

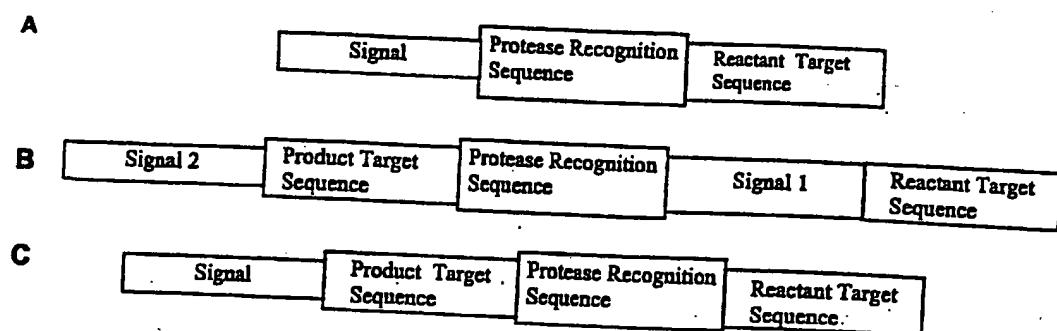


FIGURE 30

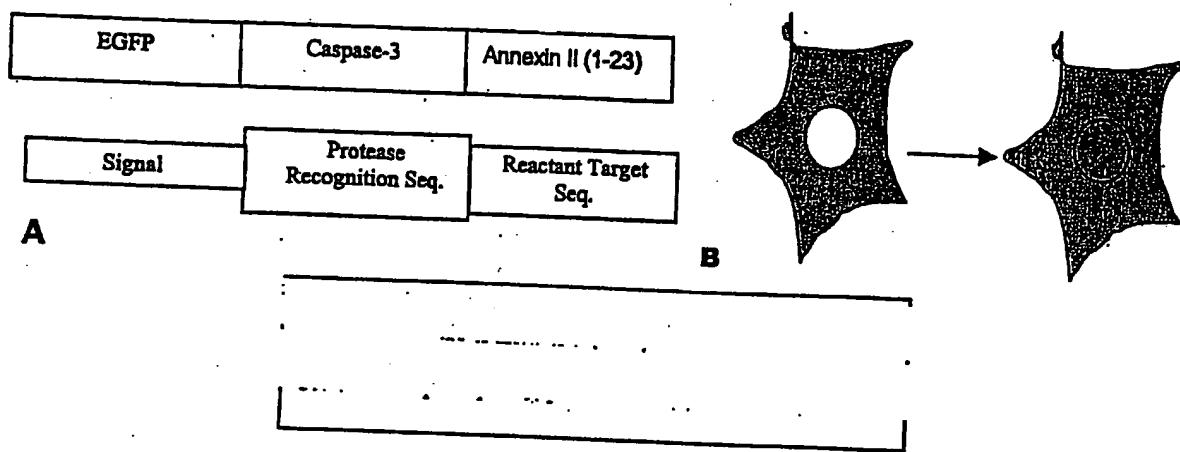


FIGURE 31

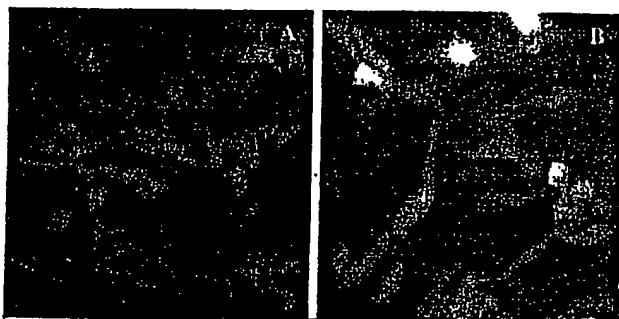
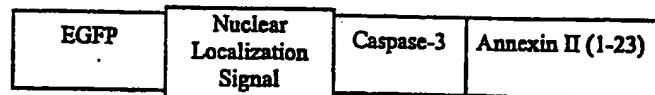
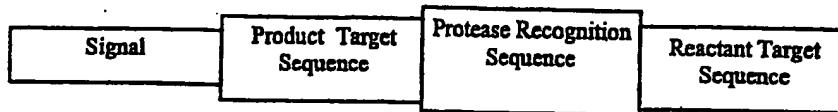


Fig 3. BHK cells transfected with DEVD-caspase biosensor.
(A) Cells before stimulation of apoptosis. (B) Another field of
cells after stimulation with 250 µg/ml cis-platin (4 h).

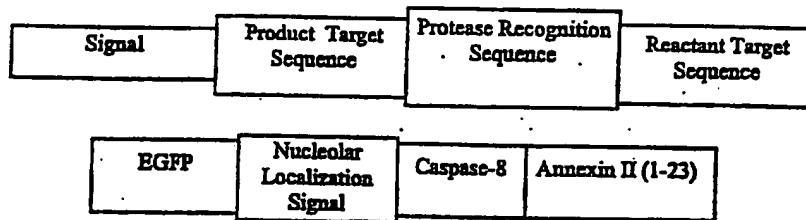
47/50



48/50

5

10



15

34

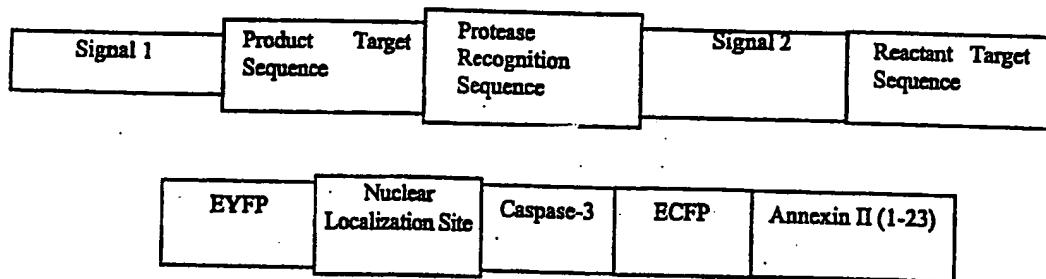


Fig. 50. Top: General design of biosensor with reactant and product containing separate targeting and signal sequences . Bottom: Specific example of this Approach—Caspase 3 biosensor with reactant targeted to cytoskeleton and product targeted to nucleus .

50/50

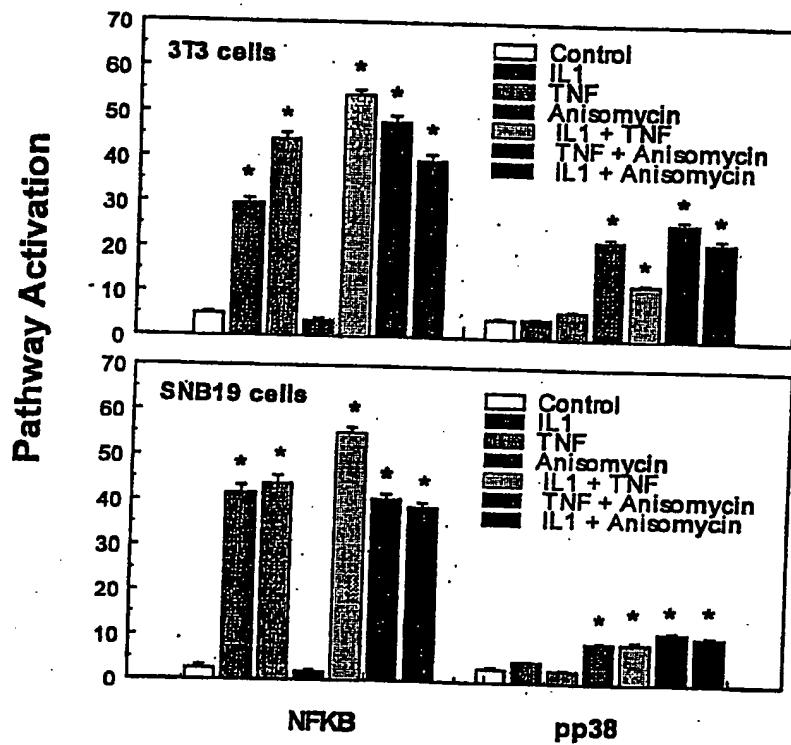


Fig. 36 Dual-labeling assay in two cell types with 3 drugs and 3 drug combinations. Treatments marked with an asterisk are different from controls at a 99% confidence level ($p < 0.01$).

SEQUENCE LISTING

<110> Giuliano, Kenneth A.
Kapur, Ravi

<120> A System for Cell Based Screening

<130> 97-022-L

<140> To Be Assigned
<141> Filed Herewith

<160> 180

<170> PatentIn Ver. 2.0

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<212> DNA

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<221> CDS
<222> (1)..(882)

<220>

<223> Description of Artificial Sequence:
GFP-DEVD-Annexin II construct

<400> 1

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Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1	5						10						15				

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	tcc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
20	25							30									

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	tcc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
35	40							45									

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50	55				60												

ctg	acc	acc	ggc	gtg	cag	tgc	tcc	agc	cgc	tac	ccc	gac	cac	atg	aag		240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
65	70				75				80								

cag	cac	gac	tcc	tcc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
85	90				95												

cgc	acc	atc	tcc	tcc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
100	105				110												

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly			
115	120				125												

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720
gga ctc aga tct ggc gcc ggc gct gga gcc gga gct ggc gcc gga gcc Gly Leu Arg Ser Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala 245 250 255	768
gac gag gtg gac ggc gcc ggc gcc gat gaa gta gat ggc gcc atg tct Asp Glu Val Asp Gly Ala Gly Ala Asp Glu Val Asp Gly Ala Met Ser 260 265 270	816
act gtc cac gaa atc ctg tgc aag ctc agc ttg gag ggt gat cat tct Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser 275 280 285	864
aca ccc cca agt gcc tat tgaatggta gcaaggcgaa ggagctgttc Thr Pro Pro Ser Ala Tyr 290	912
accgggggtgg tgccccatcct ggtcgagctg gacggcgacg taaaacggcca caagttcagc 972	
gtgtccggcg agggcgaggg cgatgccacc tacggcaagc tgaccctgaa gttcatctgc 1032	
accacccggca agctgcccgt gccctggccc accctctgtga ccaccctgtac ctacggcggt 1092	
cagtgcattca gcccgtaccc cgaccacatg aagcagcactg acttcttcaa gtccggccatg 1152	
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cgcggccgagg tgaagttcga gggcgacacc ctggtaaacc gcatcgagct gaagggcattc 1272	
gacttcaagg aggacggcaa catcctgggg cacaagctgg agtacaacta caacagccac 1332	
aacgtctata tcatggccga caagcagaag aacggcatca aggtgaactt caagatccgc 1392	

cacaacatcg aggacggcag cgtcagctc gcccaccact accagcagaa caccccccatt 1452
 ggcgacggcc ccgtgctgtc gccccacaac cactacctga gcacccagtc cgccctgagc 1512
 aaagacccca acgagaagcg cgatcacatg gtcctgctgg agttcggtac cgccgcccgg 1572
 atcactctcg gcatggacga gctgtacaag tccggactca gatctggcgc cggcgctgga 1632
 gccggagctg ggcggggagc cgacgagggtg gacggcgccg gcccgtatga agtagatggc 1692
 gccatgtcta ctgtccacga aatcctgtgc aagctcagct tggagggtga tcattctaca 1752
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1770

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<211> 294

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
GFP-DEVD-Annexin II construct

<400> 2

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1					5					10				15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
						20			25				30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
					35			40				45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
					50			55			60				

Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
					65		70		75			80			

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
					85			90		95					

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
					100			105		110					

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
					115			120		125					

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
					130		135		140						

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
					145		150		155		160				

Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
					165			170		175					

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
					180			185		190					

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
 245 250 255
 Asp Glu Val Asp Gly Ala Gly Ala Asp Glu Val Asp Gly Ala Met Ser
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 <211> 2439
 <212> DNA
 <213> Artificial Sequence

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 <221> CDS
 <222> (1)..(2436)

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 EYFP-DEVD-MAPKDM construct

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 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 384
 115 120 125
 atc gac ttc aag gag gac acc ctg gtg aac cgc atc gag ctg aag ggc
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 432
 130 135 140
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 480
 145 150 155 160
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 528
 165 170 175
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 576
 180 185 190
 ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu 624
 195 200 205
 agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 672
 210 215 220
 gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag aag
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Lys 720
 225 230 235 240
 gga gac gaa gtg gac gga gcc gac ctc agt ctt gtg gat gcg ttg aca
 Gly Asp Glu Val Asp Gly Ala Asp Leu Ser Leu Val Asp Ala Leu Thr 768
 245 250 255
 gaa cca cct cca gaa att gag gga gaa ata aag cga gac ttc atg gct
 Glu Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala 816
 260 265 270
 gcg ctg gag gca gag ccc tat gat gac atc gtg gga gaa act gtg gag
 Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu 864
 275 280 285
 aaa act gag ttt att cct ctc ctg gat ggt gat gag aaa acc ggg aac
 Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn 912
 290 295 300
 tca gag tcc aaa aag aaa ccc tgc tta gac act agc cag gtt gaa ggt
 Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly 960
 305 310 315 320
 atc cca tct tct aaa cca aca ctc cta gcc aat ggt gat cat gga atg
 Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met 1008
 325 330 335
 gag ggg aat aac act gca ggg tct cca act gac ttc ctt gaa gag aga
 Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg 1056

340	345	350	
gtg gac tat ccg gat tat cag agc agc cag aac tgg cca gaa gat gca Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala			1104
355	360	365	
agc ttt tgt ttc cag cct cag caa gtg tta gat act gac cag gct gag Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu			1152
370	375	380	
ccc ttt aac gag cac cgt gat gat ggt ttg gca gat ctg ctc ttt gtc Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val			1200
385	390	395	400
tcc agt gga ccc acg aac gct tct gca ttt aca gag cga gac aat cct Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro			1248
405	410	415	
tca gaa gac agt tac ggt atg ctt ccc tgt gac tca ttt gct tcc acg Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr			1296
420	425	430	
gct gtt gta tct cag gag tgg tct gtg gga gcc cca aac tct cca tgt Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys			1344
435	440	445	
tca gag tcc tgt gtc tcc cca gag gtt act ata gaa acc cta cag cca Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro			1392
450	455	460	
gca aca gag ctc tcc aag gca gca gaa gtg gaa tca gtg aaa gag cag Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln			1440
465	470	475	480
ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat gtg Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val			1488
485	490	495	
gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag gca Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala			1536
500	505	510	
gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata ttg Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu			1584
515	520	525	
gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc cag Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln			1632
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gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat atc Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile			1680
545	550	555	560
ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca cca Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro			1728
565	570	575	
cct atg gaa gaa att gtc cca ggc aat gat acg aca tcc ccc aaa Pro Met Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys			1776
580	585	590	

gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct gag 1824
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605

 gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc atg 1872
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620

 gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt cgc 1920
 Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640

 tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca gag 1968
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655

 gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca aca 2016
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670

 ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg gtg 2064
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685

 acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa gag 2112
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700

 aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg tct 2160
 Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720

 cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata ctt 2208
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735

 cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca gaa 2256
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750

 gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca gag 2304
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765

 gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg att 2352
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780

 gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg gaa 2400
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800

 aca aaa gta gca aca gtt cca att aaa gac aaa gga tga 2439
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 4
 <211> 812
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
EYFP-DEVD-MAPKDM construct

<400> 4

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5						10					15

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
	20					25				30					

Glu	Gly	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
	35				40					45				

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50				55					60					

Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
	65			70					75				80		

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
	85				90					95					

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
	100				105					110					

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
	115					120					125				

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130				135				140						

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
	145				150				155			160			

Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
	165					170					175				

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
	180				185					190					

Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu
	195				200				205						

Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210				215					220					

Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Lys
	225			230				235			240				

Gly	Asp	Glu	Val	Asp	Gly	Ala	Asp	Leu	Ser	Leu	Val	Asp	Ala	Leu	Thr
	245				250					255					

Glu	Pro	Pro	Pro	Glu	Ile	Glu	Gly	Glu	Ile	Lys	Arg	Asp	Phe	Met	Ala
	260				265				270						

Ala	Leu	Glu	Ala	Glu	Pro	Tyr	Asp	Asp	Ile	Val	Gly	Glu	Thr	Val	Glu
	275			280					285						

Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn
 290 295 300
 Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly
 305 310 315 320
 Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met
 325 330 335
 Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg
 340 345 350
 Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala
 355 360 365
 Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu
 370 375 380
 Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val
 385 390 395 400
 Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro
 405 410 415
 Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr
 420 425 430
 Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys
 435 440 445
 Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro
 450 455 460
 Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln
 465 470 475 480
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu
 515 520 525
 Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met

610	615	620
Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg		
625	630	635
		640
Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu		
645	650	655
Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr		
660	665	670
Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val		
675	680	685
Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu		
690	695	700
Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser		
705	710	715
720		
Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu		
725	730	735
Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu		
740	745	750
Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu		
755	760	765
Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile		
770	775	780
Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu		
785	790	795
		800
Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly		
805	810	

<210> 5
<211> 2439
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(2436)

<220>
<223> Description of Artificial Sequence:
SYFP-DEAD-MAPKDM construct

<400> 5
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

 ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

 agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

 gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag ccc 720
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Pro
 225 230 235 240

 aga gac gaa gcc gac agc gcc gac ctc agt ctt gtg gat gcg ttg aca 768
 Arg Asp Glu Ala Asp Ser Ala Asp Leu Ser Leu Val Asp Ala Leu Thr
 245 250 255

 gaa cca cct cca gaa att gag gga gaa ata aag cga gac ttc atg gct 816
 Glu Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala
 260 265 270

 gcg ctg gag gca gag ccc tat gat gac atc gtg gga gaa act gtg gag 864

Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu
 275 280 285

aaa act gag ttt att cct ctc ctg gat ggt gat gag aaa acc ggg aac 912
 Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn
 290 295 300

tca gag tcc aaa aag aaa ccc tgc tta gac act agc cag gtt gaa ggt 960
 Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly
 305 310 315 320

atc cca tct tct aaa cca aca ctc cta gcc aat ggt gat cat gga atg 1008
 Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met
 325 330 335

gag ggg aat aac act gca ggg tct cca act gac ttc ctt gaa gag aga 1056
 Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg
 340 345 350

gtg gac tat ccg gat tat cag agc agc cag aac tgg cca gaa gat gca 1104
 Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala
 355 360 365

agc ttt tgt ttc cag cct cag caa gtg tta gat act gac cag gct gag 1152
 Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu
 370 375 380

ccc ttt aac gag cac cgt gat gat ggt ttg gca gat ctg ctc ttt gtc 1200
 Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val
 385 390 395 400

tcc agt gga ccc acg aac gct tct gca ttt aca gag cga gac aat cct 1248
 Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro
 405 410 415

tca gaa gac agt tac ggt atg ctt ccc tgt gac tca ttt gct tcc acg 1296
 Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr
 420 425 430

gct gtt gta tct cag gag tgg tct gtg gga gcc cca aac tct cca tgt 1344
 Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys
 435 440 445

tca gag tcc tgt gtc tcc cca gag gtt act ata gaa acc cta cag cca 1392
 Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro
 450 455 460

gca aca gag ctc tcc aag gca gca gaa gtg gaa tca gtg aaa gag cag 1440
 Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln
 465 470 475 480

ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat gtg 1488
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495

gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag gca 1536
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510

gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata ttg 1584
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu

515	520	525	
gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc cag Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln 530	535	540	1632
gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat atc Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile 545	550	555	1680
ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca cca Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro 565	570	575	1728
cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc aaa Pro Met Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys 580	585	590	1776
gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct gag Glu Thr Glu Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu 595	600	605	1824
gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc atg Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met 610	615	620	1872
gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt cgc Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg 625	630	635	1920
tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca gag Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu 645	650	655	1968
gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca aca Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr 660	665	670	2016
ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg gtg Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val 675	680	685	2064
acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa gag Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu 690	695	700	2112
aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg tct Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser 705	710	715	2160
cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata ctt Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu 725	730	735	2208
cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca gaa Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu 740	745	750	2256
gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca gag Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu 755	760	765	2304

gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg att 2352
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780

gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg gaa 2400
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800

aca aaa gta gca aca gtt cca att aaa gac aaa gga tga 2439
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 6

<211> 812

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
EYFP-DEAD-MAPKDM construct

<400> 6

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu

195	200	205	
Ser Lys Asp Pro Asn Glu	Lys Arg Asp His Met Val	Leu Leu Glu Phe	
210	215	220	
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp	Glu Leu Tyr Lys Pro		
225	230	235	240
Arg Asp Glu Ala Asp Ser Ala Asp	Leu Ser Leu Val Asp Ala	Leu Thr	
245	250	255	
Glu Pro Pro Pro Glu Ile Glu Gly Ile Lys Arg Asp	Phe Met Ala		
260	265	270	
Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly	Glu Thr Val Glu		
275	280	285	
Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp	Glu Lys Thr Gly Asn		
290	295	300	
Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr	Ser Gln Val Glu Gly		
305	310	315	320
Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly	Asp His Gly Met		
325	330	335	
Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe	Leu Glu Glu Arg		
340	345	350	
Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp	Pro Glu Asp Ala		
355	360	365	
Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr	Asp Gln Ala Glu		
370	375	380	
Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp	Leu Leu Phe Val		
385	390	395	400
Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr	Glu Arg Asp Asn Pro		
405	410	415	
Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser	Phe Ala Ser Thr		
420	425	430	
Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro	Asn Ser Pro Cys		
435	440	445	
Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile	Glu Thr Leu Gln Pro		
450	455	460	
Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu	Ser Val Lys Glu Gln		
465	470	475	480
Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln	Thr Thr Asp Val		
485	490	495	
Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly	Pro Asp Thr Glu Ala		
500	505	510	
Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro	Asp Val Ile Leu		
515	520	525	

Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620
 Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700
 Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 7
 <211> 864
 <212> DNA
 <213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(861)

<220>

<223> Description of Artificial Sequence: F25-MEK1
construct

<400> 7

atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt	48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa	240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc	528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
 gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac acc	720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr	
225 230 235 240	
 ggc atg ccc aag aag aag ccg acg ccc atc cag ctg aac ccg gcc ccc	768
Gly Met Pro Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro	
245 250 255	
 gac ggc tct gca gtt aac ggg acc agc tct gcg gag acc aac ttg gag	816
Asp Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu	
260 265 270	
 gcc ttg cag aag aag ctg gag gag cta gag ctt gat gag cag cag tga	864
Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln	
275 280 285	

```
<210> 8
<211> 287
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: F25-MEK1
construct

<400> 8
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 86

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr
 225 230 235 240

Gly Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro
245 250 255

Asp Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu
260 265 270

Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln
275 280 285

<210> 9
<211> 876
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (873)

<220>
<223> Description of Artificial Sequence: F25-MEK2
Construct

<400> 9

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atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
   1           5                  10                15

```

ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45

```

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act    192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
      50          55          60

```

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 240

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

85	90	95	
agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			336
100	105	110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			384
115	120	125	
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			432
130	135	140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			480
145	150	155	160
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser			528
165	170	175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			576
180	185	190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			624
195	200	205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			672
210	215	220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac acc Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr			720
225	230	235	240
ggg atg ctg gcc cgg agg aag ccg gtg ctg ccg gcg ctc acc atc aac Gly Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn			768
245	250	255	
cct acc atc gcc gag ggc cca tcc cct acc agc gag ggc gcc tcc gag Pro Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu			816
260	265	270	
gca aac ctg gtg gac ctg cag aag aag ctg gag gag ctg gaa ctt gac Ala Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp			864
275	280	285	
gag cag cag taa Glu Gln Gln 290			876

<210> 10
 <211> 291
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> Description of Artificial Sequence: F25-MEK2
construct

<400> 10
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr
 225 230 235 240
 Gly Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn
 245 250 255
 Pro Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu
 260 265 270
 Ala Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp
 275 280 285
 Glu Gln Gln
 290

<210> 11
 <211> 889
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(888)

<220>
 <223> Description of Artificial Sequence: Caspase
 3-DEVD-substrate construct

<400> 11
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 576

180	185	190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195	200	205	624
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210	215	220	672
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser 225	230	235	720
gga aga agg aaa cga caa aag cga tcg gct gtt aaa tct gaa gga aag Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Val Lys Ser Glu Gly Lys 245	250	255	768
aga aag tgt gac gaa gtt gat gga att gat gaa gta gca agt act atg Arg Lys Cys Asp Glu Val Asp Gly Ile Asp Glu Val Ala Ser Thr Met 260	265	270	816
tct act gtc cac gaa atc ctg tgc aag ctc agc ttg gag ggt gtt cat Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His 275	280	285	864
tct aca ccc cca agt acc cgg atc c Ser Thr Pro Pro Ser Thr Arg Ile 290	295		889
<210> 12			
<211> 296			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Caspase 3-DEVD-substrate construct			
<400> 12			
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15			
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30			
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45			
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60			
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80			
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95			
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110			

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Val Lys Ser Glu Gly Lys
 245 250 255
 Arg Lys Cys Asp Glu Val Asp Gly Ile Asp Glu Val Ala Ser Thr Met
 260 265 270
 Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His
 275 280 285
 Ser Thr Pro Pro Ser Thr Arg Ile
 290 295

<210> 13

<211> 846

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(846)

<220>

<223> Description of Artificial Sequence: Caspase
6-VEID-substrate construct

<400> 13

atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt	48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgx cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc 720
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 gga aga agg aaa cga caa aag cga tcg aca aga ctt gtt gaa att gac 768
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Thr Arg Leu Val Glu Ile Asp
 245 250 255
 aac agt act atg agc aca gta cac gaa att tta tgt aaa tta agc tta 816
 Asn Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 260 265 270
 gaa gga gta cac agt aca cca cca agc gca 846
 Glu Gly Val His Ser Thr Pro Pro Ser Ala

275

280

<210> 14
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase
6-VEID-substrate construct

<400> 14
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
225 230 235 240
Gly Arg Arg Lys Arg Gln Lys Arg Ser Thr Arg Leu Val Glu Ile Asp
245 250 255

Asn Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
260 265 270

Glu Gly Val His Ser Thr Pro Pro Ser Ala
275 . 280

<210> 15
<211> 876
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(876)

<220>
<223> Description of Artificial Sequence: Caspase 8-VETD construct

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<400> 15
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
   1           5           10          15

```

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

```

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
          35           40           45

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tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act    192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
      50          55          60

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ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

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aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145          150          155          160

```

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

 gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

 cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

 tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

 gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc 720
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240

 gga aga agc aaa cga caa aag cga tcg tat gaa aaa gga ata cca gtt 768
 Gly Arg Ser Lys Arg Gln Lys Arg Ser Tyr Glu Lys Gly Ile Pro Val
 245 250 255

 gaa aca gac agc gaa gag caa gct tat agt act atg tct act gtc cac 816
 Glu Thr Asp Ser Glu Glu Gln Ala Tyr Ser Thr Met Ser Thr Val His
 260 265 270

 gaa atc ctg tgc aag ctc agc ttg gag ggt gtt cat tct aca ccc cca 864
 Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr Pro Pro
 275 280 285

agt gcc gga tcc
 Ser Ala Gly Ser
 290

<210> 16
 <211> 292
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase 8-VETD construct

<400> 16
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240

Gly Arg Ser Lys Arg Gln Lys Arg Ser Tyr Glu Lys Gly Ile Pro Val
 245 250 255

Glu Thr Asp Ser Glu Glu Gln Ala Tyr Ser Thr Met Ser Thr Val His
 260 265 270

Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr Pro Pro
 275 280 285

Ser Ala Gly Ser
 290

<210> 17
 <211> 906
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(906)

<220>
 <223> Description of Artificial Sequence: Cas 3-multiple
 DEVD construct

<400> 17
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	96
20 25 30	
gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	144
35 40 45	
tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	192
50 55 60	
ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	240
65 70 75 80	
cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	288
85 90 95	
agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	336
100 105 110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
115 120 125	
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
130 135 140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480
145 150 155 160	
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	528
165 170 175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	576
180 185 190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	624
195 200 205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	672
210 215 220	
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser	720
225 230 235 240	
gga aga agg aaa cga caa aag cga tcg gca ggt gac gaa gtt gat gca Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala	768
245 250 255	

ggt gac gaa gtt gat gca ggt gac gaa gtt gat gca ggt gac gaa gtt 816
 Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val
 260 265 270

gac gca ggt agt act atg tct act gtc cac gaa atc ctg tgc aag ctc 864
 Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu
 275 280 285

agc ttg gag ggt gtt cat tct aca ccc cca agt gcc gga tcc 906
 Ser Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 290 295 300

<210> 18
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cas 3-multiple
DEVD construct

<400> 18
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Glu Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala
 245 250 255
 Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val
 260 265 270
 Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu
 275 280 285
 Ser Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 290 295 300

<210> 19

<211> 906

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(885)

<220>

<223> Description of Artificial Sequence: Caspase
8-multiple VETD construct

<400> 19
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480
gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc Val Gln Leu Ala Asp His Tyr Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser 225 230 235 240	720
gga aga agg aaa cga caa aag cga tcg gca ggt gtt gaa aca gac gca Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Val Glu Thr Asp Ala 245 250 255	768
ggg gtt gaa aca gac gca ggt gtt gaa aca gac gca ggt gtt gaa aca Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr 260 265 270	816
gac gca ggt agt act atg tct act gtc cac gaa atc ctg tgc aag ctc Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu 275 280 285	864
agc ttg gag ggt gtt cat tct acaccccaa gtgccggatc c Ser Leu Glu Gly Val His Ser 290 295	906
<210> 20	
<211> 295	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Caspase 8-multiple VETD construct	
<400> 20	
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	

1	5	10	15
Val	Glu	Leu	Asp
Gly			Gly
Asp		Val	Asn
		Gly	His
20			Lys
			Phe
		Ser	Val
			Ser
			Gly
25			
			30
Glu	Gly	Gly	Asp
		Ala	Thr
		Tyr	Gly
		Lys	Leu
35		Thr	Leu
			Lys
			Phe
			Ile
40			
			45
Cys	Thr	Thr	Gly
		Lys	Leu
		Pro	Val
		Pro	Trp
		Pro	Thr
50			Leu
			Val
			Thr
			Thr
55			
			60
Leu	Cys	Tyr	Gly
	Val	Gln	Cys
		Phe	Ser
		Arg	Tyr
		Pro	Asp
		His	Met
65			Lys
70			75
75			80
Arg	His	Asp	Phe
		Phe	Lys
		Ser	Ala
		Met	Pro
85		Glu	Gly
			Tyr
		Val	Gln
			Glu
90			
			95
Arg	Thr	Ile	Phe
		Phe	Lys
		Asp	Asp
		Gly	Asn
100		Tyr	Lys
			Thr
		Arg	Ala
			Glu
105			
			110
Val	Lys	Phe	Glu
		Gly	Asp
		Thr	Leu
		Asn	Arg
115		Ile	Glu
			Leu
			Lys
			Gly
120			
			125
Ile	Asp	Phe	Lys
		Glu	Asp
		Gly	Asn
		Ile	Leu
130		Gly	
135			140
Asn	Tyr	Asn	Ser
		His	Asn
		Val	Tyr
145		Ile	Met
		Ala	Asp
		Lys	Gln
			Lys
		Asn	
150			
			160
Gly	Ile	Lys	Val
		Asn	Phe
		Gly	Lys
		Thr	Arg
		His	Asn
165		Ile	Glu
			Asp
			Gly
			Ser
170			
			175
Val	Gln	Leu	Ala
		Asp	His
		Tyr	Gln
		Gln	Asn
180			
			185
			190
Pro	Val	Leu	Leu
		Pro	Asp
		Asn	His
195		Tyr	Leu
		Ser	Thr
		Gln	Ser
			Ala
200			Leu
Ser	Lys	Asp	Pro
		Asn	Glu
		Lys	Arg
		Asp	His
210		Met	Val
		Leu	Leu
		Glu	Phe
215			
			220
Val	Thr	Ala	Ala
		Gly	Ile
		Thr	His
		Gly	Met
225		Asp	Glu
		Leu	Tyr
			Asn
			Ser
230			
			235
			240
Gly	Arg	Arg	Lys
		Arg	Gln
		Lys	Arg
		Ser	Ala
245		Gly	Val
			Glu
			Thr
			Asp
250			
			255
Gly	Val	Glu	Thr
		Asp	Ala
		Gly	Val
		Glu	Thr
260			
			265
			270
Asp	Ala	Gly	Ser
		Thr	Met
		Ser	Thr
		Val	His
275		Glu	Ile
			Leu
			Cys
			Leu
280			
			285
Ser	Leu	Glu	Gly
		Val	His
		Ser	
290			
			295

<210> 21
<211> 4833
<212> DNA
<213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(4830)

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEVD-MAP4-EBFP construct

<400> 21

atg	gtg	agc	aag	ggc	gag	gag	ctg	tcc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1							5							10		15	

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag aag Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Lys 225 230 235 240	720
gga gac gaa gtg gac gga atg gcc gac ctc agt ctt gtg gat gcg ttg Gly Asp Glu Val Asp Gly Met Ala Asp Leu Ser Leu Val Asp Ala Leu 245 250 255	768
aca gaa cca cct cca gaa att gag gga gaa ata aag cga gac ttc atg Thr Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met 260 265 270	816
gct gcg ctg gag gca gag ccc tat gat gac atc gtg gga gaa act gtg Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val 275 280 285	864
gag aaa act gag ttt att cct ctc ctg gat ggt gat gag aaa acc ggg Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly 290 295 300	912
aac tca gag tcc aaa aag aaa ccc tgc tta gac act agc cag gtt gaa Asn Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu 305 310 315 320	960
ggg atc cca tct tct aaa cca aca ctc cta gcc aat ggt gat cat gga Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly 325 330 335	1008
atg gag ggg aat aac act gca ggg tct cca act gac ttc ctt gaa gag Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu 340 345 350	1056
aga gtg gac tat ccg gat tat cag agc agc cag aac tgg cca gaa gat Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp 355 360 365	1104
gca agc ttt tgt ttc cag cct cag caa gtg tta gat act gac cag gct Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala 370 375 380	1152
gag ccc ttt aac gag cac cgt gat gat ggt ttg gca gat ctg ctc ttt Glu Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe 385 390 395 400	1200
gtc tcc agt gga ccc acg aac gct tct gca ttt aca gag cga gac aat Val Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn 405 410 415	1248
cct tca gaa gac agt tac ggt atg ctt ccc tgt gac tca ttt gct tcc Pro Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser 420 425 430	1296
acg gct gtt gta tct cag gag tgg tct gtg gga gcc cca aac tct cca Thr Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro 435 440 445	1344

tgt tca gag tcc tgt gtc tcc cca gag gtt act ata gaa acc cta cag Cys Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln 450 455 460	1392
cca gca aca gag ctc tcc aag gca gca gaa gtg gaa tca gtg aaa gag Pro Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu 465 470 475 480	1440
cag ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp 485 490 495	1488
gtg gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu 500 505 510	1536
gca gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile 515 520 525	1584
ttg gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala 530 535 540	1632
cag gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn 545 550 555 560	1680
atc ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala 565 570 575	1728
cca cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro 580 585 590	1776
aaa gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct Lys Glu Thr Glu Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro 595 600 605	1824
gag gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly 610 615 620	1872
atg gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val 625 630 635 640	1920
cgc tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr 645 650 655	1968
gag gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca Glu Val Val Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr 660 665 670	2016
aca ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu 675 680 685	2064
gtg acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa	2112

Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys
 690 695 700

gag aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg 2160
 Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met
 705 710 715 720

tct cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata 2208
 Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile
 725 730 735

ctt cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca 2256
 Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser
 740 745 750

gaa gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca 2304
 Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr
 755 760 765

gag gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg 2352
 Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu
 770 775 780

att gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg 2400
 Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu
 785 790 795 800

gaa aca aaa gta gca aca gtt cca att aaa gac aaa gga act gta cag 2448
 Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly Thr Val Gln
 805 810 815

act gaa gaa aaa cca cgt gaa gac tcc cag tta gca tct atg cag cac 2496
 Thr Glu Glu Lys Pro Arg Glu Asp Ser Gln Leu Ala Ser Met Gln His
 820 825 830

aag gga cag tca aca gta cct cct tgc acg gct tca cca gaa cca gtc 2544
 Lys Gly Gln Ser Thr Val Pro Pro Cys Thr Ala Ser Pro Glu Pro Val
 835 840 845

aaa gct gca gaa caa atg tct acc tta cca ata gat gca cct tct cca 2592
 Lys Ala Ala Glu Gln Met Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro
 850 855 860

tta gag aac tta gag cag aag gaa acg cct ggc agc cag cct tct gag 2640
 Leu Glu Asn Leu Glu Gln Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu
 865 870 875 880

cct tgc tca gga gta tcc cgg caa gaa gca aag gct gct gta ggt 2688
 Pro Cys Ser Gly Val Ser Arg Gln Glu Ala Lys Ala Ala Val Gly
 885 890 895

gtg act gga aat gac atc act acc ccc cca aac aag gag cca cca cca 2736
 Val Thr Gly Asn Asp Ile Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro
 900 905 910

agc cca gaa aag aaa gca aag cct ttg gcc acc act caa cct gca aag 2784
 Ser Pro Glu Lys Lys Ala Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys
 915 920 925

act tca aca tcg aaa gcc aaa aca cag ccc act tct ctc cct aag caa 2832
 Thr Ser Thr Ser Lys Ala Lys Thr Gln Pro Thr Ser Leu Pro Lys Gln

930	935	940	
cca gct ccc acc acc tct ggt ggg ttg aat aaa aaa ccc atg agc ctc Pro Ala Pro Thr Thr Ser Gly Gly Leu Asn Lys Lys Pro Met Ser Leu			2880
945	950	955	960
gcc tca ggc tca gtg cca gct gcc cca cac aaa cgc cct gct gct gcc Ala Ser Gly Ser Val Pro Ala Ala Pro His Lys Arg Pro Ala Ala Ala			2928
965	970	975	
act gct act gcc agg cct tcc acc cta cct gcc aga gac gtg aag cca Thr Ala Thr Ala Arg Pro Ser Thr Leu Pro Ala Arg Asp Val Lys Pro			2976
980	985	990	
aag cca att aca gaa gct aag gtt gcc gaa aag cgg acc tct cca tcc Lys Pro Ile Thr Glu Ala Lys Val Ala Glu Lys Arg Thr Ser Pro Ser			3024
995	1000	1005	
aag cct tca tct gcc cca gcc ctc aaa cct gga cct aaa acc acc cca Lys Pro Ser Ser Ala Pro Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro			3072
1010	1015	1020	
acc gtt tca aaa gcc aca tct ccc tca act ctt gtt tcc act gga cca Thr Val Ser Lys Ala Thr Ser Pro Ser Thr Leu Val Ser Thr Gly Pro			3120
1025	1030	1035	1040
agt agt aga agt cca gct aca act ctg cct aag agg cca acc agc atc Ser Ser Arg Ser Pro Ala Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile			3168
1045	1050	1055	
aag act gag ggg aaa cct gct gat gtc aaa agg atg act gct aag tct Lys Thr Glu Gly Lys Pro Ala Asp Val Lys Arg Met Thr Ala Lys Ser			3216
1060	1065	1070	
gcc tca gct gac ttg agt cgc tca aag acc acc tct gcc agt tct gtg Ala Ser Ala Asp Leu Ser Arg Ser Lys Thr Thr Ser Ala Ser Ser Val			3264
1075	1080	1085	
aag aga aac acc act ccc act ggg gca gca ccc cca gca ggg atg act Lys Arg Asn Thr Thr Pro Thr Gly Ala Ala Pro Pro Ala Gly Met Thr			3312
1090	1095	1100	
tcc act cga gtc aag ccc atg tct gca cct agc cgc tct tct ggg gct Ser Thr Arg Val Lys Pro Met Ser Ala Pro Ser Arg Ser Ser Gly Ala			3360
1105	1110	1115	1120
ctt tct gtg gac aag aag ccc act tcc act aag cct agc tcc tct gct Leu Ser Val Asp Lys Lys Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala			3408
1125	1130	1135	
ccc agg gtg agc cgc ctg gcc aca act gtt tct gcc cct gac ctg aag Pro Arg Val Ser Arg Leu Ala Thr Thr Val Ser Ala Pro Asp Leu Lys			3456
1140	1145	1150	
agt gtt cgc tcc aag gtc ggc tct aca gaa aac atc aaa cac cag cct Ser Val Arg Ser Lys Val Gly Ser Thr Glu Asn Ile Lys His Gln Pro			3504
1155	1160	1165	
gga gga ggc cgg gcc aaa gta gag aaa aaa aca gag gca gct acc aca Gly Gly Arg Ala Lys Val Glu Lys Lys Thr Glu Ala Ala Thr Thr			3552
1170	1175	1180	

gct ggg aag cct gaa cct aat gca gtc act aaa gca gcc ggc tcc att Ala Gly Lys Pro Glu Pro Asn Ala Val Thr Lys Ala Ala Gly Ser Ile 1185 1190 1195 1200	3600
gcg agt gca cag aaa ccg cct gct ggg aaa gtc cag ata gta tcc aaa Ala Ser Ala Gln Lys Pro Pro Ala Gly Lys Val Gln Ile Val Ser Lys 1205 1210 1215	3648
aaa gtg agc tac agt cat att caa tcc aag tgt gtt tcc aag gac aat Lys Val Ser Tyr Ser His Ile Gln Ser Lys Cys Val Ser Lys Asp Asn 1220 1225 1230	3696
att aag cat gtc cct gga tgt ggc aat gtt cag att cag aac aag aaa Ile Lys His Val Pro Gly Cys Gly Asn Val Gln Ile Gln Asn Lys Lys 1235 1240 1245	3744
gtg gac ata tcc aag gtc tcc tcc aag tgt ggg tcc aaa gct aat atc Val Asp Ile Ser Lys Val Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile 1250 1255 1260	3792
aag cac aag cct ggt gga gga gat gtc aag att gaa agt cag aag ttg Lys His Lys Pro Gly Gly Asp Val Lys Ile Glu Ser Gln Lys Leu 1265 1270 1275 1280	3840
aac ttc aag gag aag gcc caa gcc aaa gtg gga tcc ctt gat aac gtt Asn Phe Lys Glu Lys Ala Gln Ala Lys Val Gly Ser Leu Asp Asn Val 1285 1290 1295	3888
ggc cac ttt cct gca gga ggt gcc gtg aag act gag ggc ggt ggc agt Gly His Phe Pro Ala Gly Gly Ala Val Lys Thr Glu Gly Gly Ser 1300 1305 1310	3936
gag gcc ctt ccg tgt cca ggc ccc ccc gct ggg gag gag cca gtc atc Glu Ala Leu Pro Cys Pro Gly Pro Pro Ala Gly Glu Glu Pro Val Ile 1315 1320 1325	3984
cct gag gct gcg cct gac cgt ggc gcc cct act tca gcc agt ggc ctc Pro Glu Ala Ala Pro Asp Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu 1330 1335 1340	4032
agt ggc cac acc acc ctg tca ggg ggt ggt gac caa agg gag ccc cag Ser Gly His Thr Thr Leu Ser Gly Gly Asp Gln Arg Glu Pro Gln 1345 1350 1355 1360	4080
acc ttg gac agc cag atc cag gag aca agc atc atg gtg agc aag ggc Thr Leu Asp Ser Gln Ile Gln Glu Thr Ser Ile Met Val Ser Lys Gly 1365 1370 1375	4128
gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly 1380 1385 1390	4176
gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp 1395 1400 1405	4224
gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys 1410 1415 1420	4272

ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val 1425 1430 1435 1440	4320
cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe 1445 1450 1455	4368
aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe 1460 1465 1470	4416
aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly 1475 1480 1485	4464
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1490 1495 1500	4512
gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His 1505 1510 1515 1520	4560
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 1525 1530 1535	4608
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 1540 1545 1550	4656
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 1555 1560 1565	4704
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 1570 1575 1580	4752
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 1585 1590 1595 1600	4800
atc act ctc ggc atg gac gag ctg tac aag tag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 1605 1610	4833
<210> 22	
<211> 1610	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: EYFP-DEVD-MAP4-EBFP construct	
<400> 22	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Glu Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Lys
 225 230 235 240

Gly Asp Glu Val Asp Gly Met Ala Asp Leu Ser Leu Val Asp Ala Leu
 245 250 255

Thr Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met
 260 265 270

Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val
 275 280 285

Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly
 290 295 300

Asn Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu
 305 310 315 320

Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly
 325 330 335

Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu
 340 345 350
 Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp
 355 360 365
 Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala
 370 375 380
 Glu Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe
 385 390 395 400
 Val Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn
 405 410 415
 Pro Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser
 420 425 430
 Thr Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro
 435 440 445
 Cys Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln
 450 455 460
 Pro Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu
 465 470 475 480
 Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp
 485 490 495
 Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu
 500 505 510
 Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile
 515 520 525
 Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala
 530 535 540
 Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn
 545 550 555 560
 Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala
 565 570 575
 Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro
 580 585 590
 Lys Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro
 595 600 605
 Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly
 610 615 620
 Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val
 625 630 635 640
 Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr
 645 650 655
 Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr

660

665

670

Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu
 675 680 685

Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys
 690 695 700

Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met
 705 710 715 720

Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile
 725 730 735

Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser
 740 745 750

Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr
 755 760 765

Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu
 770 775 780

Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu
 785 790 795 800

Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly Thr Val Gln
 805 810 815

Thr Glu Glu Lys Pro Arg Glu Asp Ser Gln Leu Ala Ser Met Gln His
 820 825 830

Lys Gly Gln Ser Thr Val Pro Pro Cys Thr Ala Ser Pro Glu Pro Val
 835 840 845

Lys Ala Ala Glu Gln Met Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro
 850 855 860

Leu Glu Asn Leu Glu Gln Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu
 865 870 875 880

Pro Cys Ser Gly Val Ser Arg Gln Glu Glu Ala Lys Ala Ala Val Gly
 885 890 895

Val Thr Gly Asn Asp Ile Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro
 900 905 910

Ser Pro Glu Lys Lys Ala Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys
 915 920 925

Thr Ser Thr Ser Lys Ala Lys Thr Gln Pro Thr Ser Leu Pro Lys Gln
 930 935 940

Pro Ala Pro Thr Thr Ser Gly Gly Leu Asn Lys Lys Pro Met Ser Leu
 945 950 955 960

Ala Ser Gly Ser Val Pro Ala Ala Pro His Lys Arg Pro Ala Ala Ala
 965 970 975

Thr Ala Thr Ala Arg Pro Ser Thr Leu Pro Ala Arg Asp Val Lys Pro
 980 985 990

Lys Pro Ile Thr Glu Ala Lys Val Ala Glu Lys Arg Thr Ser Pro Ser
 995 1000 1005
 Lys Pro Ser Ser Ala Pro Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro
 1010 1015 1020
 Thr Val Ser Lys Ala Thr Ser Pro Ser Thr Leu Val Ser Thr Gly Pro
 1025 1030 1035 1040
 Ser Ser Arg Ser Pro Ala Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile
 1045 1050 1055
 Lys Thr Glu Gly Lys Pro Ala Asp Val Lys Arg Met Thr Ala Lys Ser
 1060 1065 1070
 Ala Ser Ala Asp Leu Ser Arg Ser Lys Thr Thr Ser Ala Ser Ser Val
 1075 1080 1085
 Lys Arg Asn Thr Thr Pro Thr Gly Ala Ala Pro Pro Ala Gly Met Thr
 1090 1095 1100
 Ser Thr Arg Val Lys Pro Met Ser Ala Pro Ser Arg Ser Ser Gly Ala
 1105 1110 1115 1120
 Leu Ser Val Asp Lys Lys Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala
 1125 1130 1135
 Pro Arg Val Ser Arg Leu Ala Thr Thr Val Ser Ala Pro Asp Leu Lys
 1140 1145 1150
 Ser Val Arg Ser Lys Val Gly Ser Thr Glu Asn Ile Lys His Gln Pro
 1155 1160 1165
 Gly Gly Gly Arg Ala Lys Val Glu Lys Lys Thr Glu Ala Ala Thr Thr
 1170 1175 1180
 Ala Gly Lys Pro Glu Pro Asn Ala Val Thr Lys Ala Ala Gly Ser Ile
 1185 1190 1195 1200
 Ala Ser Ala Gln Lys Pro Pro Ala Gly Lys Val Gln Ile Val Ser Lys
 1205 1210 1215
 Lys Val Ser Tyr Ser His Ile Gln Ser Lys Cys Val Ser Lys Asp Asn
 1220 1225 1230
 Ile Lys His Val Pro Gly Cys Gly Asn Val Gln Ile Gln Asn Lys Lys
 1235 1240 1245
 Val Asp Ile Ser Lys Val Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile
 1250 1255 1260
 Lys His Lys Pro Gly Gly Asp Val Lys Ile Glu Ser Gln Lys Leu
 1265 1270 1275 1280
 Asn Phe Lys Glu Lys Ala Gln Ala Lys Val Gly Ser Leu Asp Asn Val
 1285 1290 1295
 Gly His Phe Pro Ala Gly Ala Val Lys Thr Glu Gly Gly Ser
 1300 1305 1310

Glu Ala Leu Pro Cys Pro Gly Pro Pro Ala Gly Glu Glu Pro Val Ile
 1315 1320 1325
 Pro Glu Ala Ala Pro Asp Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu
 1330 1335 1340
 Ser Gly His Thr Thr Leu Ser Gly Gly Asp Gln Arg Glu Pro Gln
 1345 1350 1355 1360
 Thr Leu Asp Ser Gln Ile Gln Glu Thr Ser Ile Met Val Ser Lys Gly
 1365 1370 1375
 Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
 1380 1385 1390
 Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
 1395 1400 1405
 Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
 1410 1415 1420
 Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val
 1425 1430 1435 1440
 Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
 1445 1450 1455
 Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 1460 1465 1470
 Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
 1475 1480 1485
 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 1490 1495 1500
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His
 1505 1510 1515 1520
 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 1525 1530 1535
 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 1540 1545 1550
 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 1555 1560 1565
 Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 1570 1575 1580
 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 1585 1590 1595 1600
 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1605 1610

<210> 23
 <211> 978
 <212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(978)

<220>

<223> Description of Artificial Sequence:
GFP-nucleolus-Caspase 8-annexin II construct

<400> 23

atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt	48
Met Ala Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa	240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc	528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	

195

200

205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc	720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser	
225 230 235 240	

gga aga aaa cgt ata cgt act tac ctc aag tcc tgc agg cgg atg aaa 768
Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys
245 250 255

aga agt ggt ttt gag atg tct cga cct att cct tcc cac ctt act cga 816
Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg
260 265 270

tcg gca ggt gtt gaa aca gac gca ggt gtt gaa aca gac gca ggt gtt 864
 Ser Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val
 275 280 285

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gaa aca gac gca ggt gtt gaa aca gac gca ggt agt act atg tct act 912
Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Ser Thr Met Ser Thr
    290          295          300

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gtc cac gaa atc ctg tgc aag ctc agc ttg gag ggt gtt cat tct aca 960
 Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr
 305 310 315 320

ccc cca agt gcc gga tcc 978
Pro Pro Ser Ala Gly Ser
325

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<210> 24
<211> 326
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
GFP-nucleolus-Caspase 8-annexin II construct

<400> 24
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
145	150	155
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser		
165	170	175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
180	185	190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
195	200	205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
210	215	220
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser		
225	230	235
Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys		
245	250	255
Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg		
260	265	270
Ser Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val		
275	280	285
Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Ser Thr Met Ser Thr		
290	295	300
Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr		
305	310	315
Pro Pro Ser Ala Gly Ser		
325		

<210> 25
 <211> 948
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(948)

<220>
 <223> Description of Artificial Sequence:
 GFP-nucleolus-Caspase 3-annexin II construct

<400> 25
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
Met Ala Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc 576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc 720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
225 230 235 240

gga aga aaa cgt ata cgt act tac ctc aag tcc tgc agg cgg atg aaa 768
 Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys
 245 250 255

aga agt ggt ttt gag atg tct cga cct att cct tcc cac ctt act cga 816
 Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg
 260 265 270

tcg tat gaa aaa gga ata cca gtt gaa aca gac agc gaa gag caa gct 864
 Ser Tyr Glu Lys Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Ala
 275 280 285

tat agt act atg tct act gtc cac gaa atc ctg tgc aag ctc agc ttg 912
 Tyr Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 290 295 300

gag ggt gtt cat tct aca ccc cca agt gcc gga tcc 948
 Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 305 310 315

<210> 26

<211> 316

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 GFP-nucleolus-Caspase 3-annexin II construct

<400> 26

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20	25	30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35	40	45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50	55	60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
65	70	75	80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85	90	95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100	105	110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys
 245 250 255
 Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg
 260 265 270
 Ser Tyr Glu Lys Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Ala
 275 280 285
 Tyr Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 290 295 300
 Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 305 310 315

<210> 27
<211> 2088
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1041)

<220>
<223> Description of Artificial Sequence:
NLS-Fred25-synaptobrevin construct

<400> 27
atg aga aga aaa cga caa aag gct agc aaa gga gaa gaa ctc ttc act 48
Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
1 5 10 15

gga gtt gtc cca att ctt gtt gaa tta gat ggt gat gtt aac ggc cac 96
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 20 25 30

```

aag ttc tct gtc agt gga gag ggt gaa ggt gat gca aca tac gga aaa 144
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
            35          40          45

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ctt acc ctg aag ttc atc tgc act act ggc aaa ctg cct gtt cca tgg 192
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 50 55 60

cca aca cta gtc act act ctg tgc tat ggt gtt caa tgc ttt tca aga 240
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
 65 70 75 80
 tac ccg gat cat atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc 288
 Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 85 90 95
 gaa ggt tat gta cag gaa agg acc atc ttc ttc aaa gat gac ggc aac 336
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 100 105 110
 tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat 384
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 115 120 125
 aga atc gag tta aaa ggt att gac ttc aag gaa gat ggc aac att ctg 432
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 130 135 140
 gga cac aaa ttg gaa tac aac tat aac tca cac aat gta tac atc atg 480
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 145 150 155 160
 gca gac aaa caa aag aat gga atc aaa gtg aac ttc aag acc cgc cac 528
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 165 170 175
 aac att gaa gat gga agc gtt caa cta gca gac cat tat caa caa aat 576
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 180 185 190
 act cca att ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg 624
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 195 200 205
 tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag aga gac cac 672
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 210 215 220
 atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca cat ggc atg 720
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 225 230 235 240
 gat gaa ctg tac aac acc ggt atg tct aca ggt cca act gct gcc act 768
 Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Pro Thr Ala Ala Thr
 245 250 255
 ggc agt aat cga aga ctt cag cag aca caa aat caa gta gat gag gtg 816
 Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln Val Asp Glu Val
 260 265 270
 gtg gac ata atg cga gtt aac gtg gac aag gtt ctg gaa aga gac cag 864
 Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu Glu Arg Asp Gln
 275 280 285
 aag ctc tct gag tta gac gac cgt gca gac gca ctg cag gca ggc gct 912
 Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu Gln Ala Gly Ala
 290 295 300
 tct caa ttt gaa acg agc gca gac aag ttg aag agg aaa tat tgg tgg 960

Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg Lys Tyr Trp Trp
 305 310 315 320
 aag aat tgc aag atg tgg gca atc ggg att act gtt ctg gtt atc ttc 1008
 Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Thr Val Leu Val Ile Phe
 325 330 335
 atc atc atc atc gtg tgg gtt gtc tct tca tgaatgagaa gaaaacgaca 1061
 Ile Ile Ile Ile Ile Val Trp Val Val Ser Ser
 340 345
 aaaggcttagc aaaggagaag aactcttac tggagttgtc ccaattcttg ttgaattaga 1121
 tgggtatgtt aacggccaca agttctctgt cagtggagag ggtgaaggtg atgcaacata 1181
 cggaaaacctt accctgaagt tcatctgcac tactggcaaa ctgcctgttc catggccaac 1241
 actagtcact actctgtgtc atgggtgttca atgctttca agatacccg atcatatgaa 1301
 acggcatgac ttttcaaga gtgccatgcc cgaaggttat gtacaggaaa ggaccatctt 1361
 cttcaaagat gacggcaact acaagacacg tgctgaagtc aagtttgaag gtgataccct 1421
 tgttaataga atcgagttaa aaggtattga cttcaaggaa gatggcaaca ttctgggaca 1481
 caaattggaa tacaactata actcacacaa tgtatacatc atggcagaca aacaaaagaa 1541
 tggaatcaaa gtgaacttca agacccgcca caacattgaa gatggagcg ttcaactagc 1601
 agaccattat caacaaaata ctccaattgg cgatggccct gtcctttac cagacaacca 1661
 ttacctgtcc acacaatctg ccctttcgaa agatcccaac gaaaagagag accacatgg 1721
 ccttcttgag tttgtaacag ctgctggat tacacatggc atggatgaac tgtacaacac 1781
 cggtatgtct acaggtccaa ctgctgccac tggcagtaat cgaagacttc agcagacaca 1841
 aaatcaagta gatgaggtgg tggacataat gcgagtaac gtggacaagg ttctggaaag 1901
 agaccagaag ctctctgagt tagacgaccg tgcagacgca ctgcaggcag ggccttctca 1961
 atttgaaacg agcgcagcca agttgaagag gaaatattgg tggagaatt gcaagatgtg 2021
 ggcaatcggg attactgttc tggttatctt catcatcatc atcatcgtgt gggttgtctc 2081
 ttcatga 2088

 <210> 28
 <211> 347
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 NLS-Fred25-synaptobrevin construct

 <400> 28
 Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
 1 5 10 15

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 20 25 30

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 35 40 45

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 50 55 60

Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
 65 70 75 80

Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 85 90 95

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 100 105 110

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 115 120 125

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 130 135 140

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 145 150 155 160

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 165 170 175

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 180 185 190

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 195 200 205

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 210 215 220

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 225 230 235 240

Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Pro Thr Ala Ala Thr
 245 250 255

Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln Val Asp Glu Val
 260 265 270

Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu Glu Arg Asp Gln
 275 280 285

Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu Gln Ala Gly Ala
 290 295 300

Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg Lys Tyr Trp Trp
 305 310 315 320

Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Thr Val Leu Val Ile Phe
 325 330 335

Ile Ile Ile Ile Ile Val Trp Val Val Ser Ser

340

345

<210> 29
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (1050)

<220>
<223> Description of Artificial Sequence:
NLS-Fred2S-cellubrevin construct

<400> 39

atg aga aga aaa cga caa aag gct agc aaa gga gaa gaa ctc ttc act 48
 Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
 1 5 10 15

gga gtt gtc cca att ctt gtt gaa tta gat ggt gat gtt aac ggc cac 96
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 20 25 30

aag ttc tct gtc agt gga gag ggt gaa ggt gat gca aca tac gga aaa	144	
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys		
35	40	45

ctt acc ctg aag ttc atc tgc act act ggc aaa ctg cct gtt cca tgg 192
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 50 55 60

cca	aca	cta	gtc	act	act	ctg	tgc	tat	ggt	gtt	caa	tgc	ttt	tca	aga	240
Pro	Thr	Leu	Val	Thr	Thr	Leu	Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	
65				70						75					80	

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tac ccg gat cat atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc 288
Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
          85           90           95

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gaa ggt tat gta cag gaa agg acc atc ttc ttc aaa gat gac ggc aac	336
Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn	
100 105 110	

tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat 384
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 115 120 125

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aga atc gag tta aaa ggt att gac ttc aag gaa gat ggc aac att ctg 432
Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
    130          135          140

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gga cac aaa ttg gaa tac aac tat aac tca cac aat gta tac atc atg 480
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 145 150 155 160

gca gac aaa caa aag aat gga atc aaa gtg aac ttc aag acc cgc cac 528
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 165 170 175

aac att gaa gat gga agc gtt caa cta gca gac cat tat caa caa aat 576
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 180 185 190

act cca att ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg 624
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 195 200 205

tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag aga gac cac 672
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 210 215 220

atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca cat ggc atg 720
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 225 230 235 240

gat gaa ctg tac aac acc ggt atg tct aca ggt gtg cct tcg ggg tca 768
 Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Val Pro Ser Gly Ser
 245 250 255

agt gct gcc act ggc agt aat cga aga ctc cag cag aca caa aat caa 816
 Ser Ala Ala Thr Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln
 260 265 270

gta gat gag gtg gtt gac atc atg aga gtc aat gtg gat aag gtg tta 864
 Val Asp Glu Val Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu
 275 280 285

gaa aga gac cag aag ctc tcg gag cta gat gac cgc gca gat gca ctg 912
 Glu Arg Asp Gln Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu
 290 295 300

cag gca ggt gcc tcg cag ttt gaa aca agt gct gcc aag ttg aag aga 960
 Gln Ala Gly Ala Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg
 305 310 315 320

aag tat tgg tgg aag aac tgc aag atg tgg gcg ata ggg atc agt gtc 1008
 Lys Tyr Trp Trp Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Ser Val
 325 330 335

ctg gtg atc att gtc atc atc atc gtg tgg tgt gtc tct 1050
 Leu Val Ile Ile Val Ile Ile Ile Val Trp Cys Val Ser
 340 345 350

taaaatgagaa gaaaacgaca aaaggcttagc aaaggagaag aactttcac tggagttgtc 1110
 ccaattcttg ttgaattaga tggatgttt aacggccaca agttctctgt cagtggagag 1170
 ggtgaaggtg atgcaacata cggaaaactt accctgaagt tcatctgcac tactggcaaa 1230
 ctgcctgttc catggccaac actagtcaact actctgtgct atgggttca atgctttca 1290
 agatacccg atcatatgaa acggcatgac ttttcaaga gtgccatgcc cgaaggttat 1350
 gtacaggaaa ggaccatctt cttcaaagat gacggcaact acaagacacg tgctgaagtc 1410
 aagtttgaag gtgataccct tgtaataga atcgagttaa aaggtattga cttcaaggaa 1470
 gatggcaaca ttctggaca caaattggaa tacaactata actcacacaa tgtatacatc 1530
 atggcagaca aacaaaagaa tggaatcaa gtgaacttca agacccgcca caacattgaa 1590

gatggaagcg ttcaactagc agaccattat caacaaaata ctccaattgg cgatggccct 1650
 gtcctttac cagacaacca ttacctgtcc acacaatctg ccctttcgaa agatccaaac 1710
 gaaaagagag accacatggt cttcttgag tttgtAACAG ctgtggat tacacatggc 1770
 atggatgaac tgtacaacac cggtatgtct acagggtgtgc cttcggggtc aagtgtgcc 1830
 actggcagta atcgaagact ccagcagaca caaaatcaag tagatgaggt gggtgacatc 1890
 atgagagtca atgtggataa ggtgttagaa agagaccaga agctctcgga gctagatgac 1950
 cgcgcagatg cactgcaggc aggtgcctcg cagttgaaa caagtgtgc caagttgaag 2010
 agaaagtatt ggtggaagaa ctgcaagatg tggcgatag ggatcagtgt cctggtgatc 2070
 attgtcatca tcacatcatcg gtggtgtgtc tcttaa

2106

<210> 30

<211> 350

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
NLS-Fred25-cellubrevin construct

<400> 30

Met	Arg	Arg	Lys	Arg	Gln	Lys	Ala	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr
1					5				10					15	

Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His
20						25				30					

Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys
35					40				45				

Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp
50					55				60						

Pro	Thr	Leu	Val	Thr	Thr	Leu	Cys	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg
65					70				75			80			

Tyr	Pro	Asp	His	Met	Lys	Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro
				85				90				95			

Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn
100					105				110						

Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Asp	Thr	Leu	Val	Asn
				115			120			125				

Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu
	130				135				140						

Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met
145					150				155			160			

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His

165	170	175
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn		
180	185	190
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu		
195	200	205
Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His		
210	215	220
Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met		
225	230	235
Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Val Pro Ser Gly Ser		
245	250	255
Ser Ala Ala Thr Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln		
260	265	270
Val Asp Glu Val Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu		
275	280	285
Glu Arg Asp Gln Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu		
290	295	300
Gln Ala Gly Ala Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg		
305	310	315
Lys Tyr Trp Trp Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Ser Val		
325	330	335
Leu Val Ile Ile Val Ile Ile Ile Val Trp Cys Val Ser		
340	345	350

<210> 31
 <211> 3171
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(3168)

<220>
 <223> Description of Artificial Sequence:
 NLS-EYFP-MAPKDM-EBFP construct

<400> 31																
atg agg ccc aga aga aag gtg agc aag ggc gag gag ctg ttc acc ggg 48																
Met	Arg	Pro	Arg	Arg	Lys	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	
1																
			5						10					15		
gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag 96																
Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	
			20				25				30					
ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg 144																
Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	
			35				40				45					

acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc 192
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 50 55 60

acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac 240
 Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr
 65 70 75 80

ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa 288
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
 85 90 95

ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac 336
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 100 105 110

aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc 384
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 115 120 125

atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg 432
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 130 135 140

cac aag ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc 480
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 145 150 155 160

gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac 528
 Asp Lys Gln Lys Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
 165 170 175

atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc 576
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 180 185 190

ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc 624
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 195 200 205

tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg 672
 Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 210 215 220

gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc gcc atg gac 720
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 225 230 235 240

gag ctg tac aag aag gga gac gaa gtg gac gga gcc gac ctc agt ctt 768
 Glu Leu Tyr Lys Lys Gly Asp Glu Val Asp Gly Ala Asp Leu Ser Leu
 245 250 255

gtg gat ggc ttg aca gaa cca cct cca gaa att gag gga gaa ata aag 816
 Val Asp Ala Leu Thr Glu Pro Pro Glu Ile Glu Gly Glu Ile Lys
 260 265 270

cga gac ttc atg gct gcg ctg gag gca gag ccc tat gat gac atc gtg 864
 Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val
 275 280 285

gga gaa act gtg gag aaa act gag ttt att cct ctc ctg gat ggt gat 912
 Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp
 290 295 300

gag aaa acc ggg aac tca gag tcc aaa aag aaa ccc tgc tta gac act 960
 Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr
 305 310 315 320

agc cag gtt gaa ggt atc cca tct tct aaa cca aca ctc cta gcc aat 1008
 Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn
 325 330 335

ggt gat cat gga atg gag ggg aat aac act gca ggg tct cca act gac 1056
 Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp
 340 345 350

ttc ctt gaa gag aga gtg gac tat ccg gat tat cag agc agc cag aac 1104
 Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn
 355 360 365

tgg cca gaa gat gca agc ttt tgt ttc cag cct cag caa gtg tta gat 1152
 Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp
 370 375 380

act gac cag gct gag ccc ttt aac gag cac cgt gat gat ggt ttg gca 1200
 Thr Asp Gln Ala Glu Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala
 385 390 395 400

gat ctg ctc ttt gtc tcc agt gga ccc acg aac gct tct gca ttt aca 1248
 Asp Leu Leu Phe Val Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr
 405 410 415

gag cga gac aat cct tca gaa gac agt tac ggt atg ctt ccc tgt gac 1296
 Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp
 420 425 430

tca ttt gct tcc acg gct gtt gta tct cag gag tgg tct gtg gga gcc 1344
 Ser Phe Ala Ser Thr Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala
 435 440 445

cca aac tct cca tgt tca gag tcc tgt gtc tcc cca gag gtt act ata 1392
 Pro Asn Ser Pro Cys Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile
 450 455 460

gaa acc cta cag cca gca aca gag ctc tcc aag gca gca gaa gtg gaa 1440
 Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu
 465 470 475 480

tca gtg aaa gag cag ctg cca gct aaa gca ttg gaa acg atg gca gag 1488
 Ser Val Lys Glu Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu
 485 490 495

cag acc act gat gtg gtg cac tct cca tcc aca gac aca aca cca ggc 1536
 Gln Thr Thr Asp Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly
 500 505 510

cca gac aca gag gca gca ctg gct aaa gac ata gaa gag atc acc aag 1584
 Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys
 515 520 525

cca gat gtg ata ttg gca aat gtc acg cag cca tct act gaa tcg gat 1632

Pro Asp Val Ile Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp
 530 535 540

atg ttc ctg gcc cag gac atg gaa cta ctc aca gga aca gag gca ggc
 Met Phe Leu Ala Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala
 545 550 555 560

cac gct aac aat atc ata ttg cct aca gaa cca gac gaa tct tca acc
 His Ala Asn Asn Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr
 565 570 575

aag gat gta gca cca cct atg gaa gaa gaa att gtc cca ggc aat gat
 Lys Asp Val Ala Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp
 580 585 590

acg aca tcc ccc aaa gaa aca gag aca aca ctt cca ata aaa atg gac
 Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp
 595 600 605

ttg gca cca cct gag gat gtg tta ctt acc aaa gaa aca gaa cta gcc
 Leu Ala Pro Pro Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala
 610 615 620

cca gcc aag ggc atg gtt tca ctc tca gaa ata gaa gag gct ctg gca
 Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala
 625 630 635 640

aag aat gat gtt cgc tct gca gaa ata cct gtg gct cag gag aca gtg
 Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val
 645 650 655

gtc tca gaa aca gag gtg gtc ctg gca aca gaa gtg gta ctg ccc tca
 Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser
 660 665 670

gat ccc ata aca aca ttg aca aag gat gtg aca ctc ccc tta gaa gca
 Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala
 675 680 685

gag aga ccg ttg gtg acg gac atg act cca tct ctg gaa aca aca gaa atg
 Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met
 690 695 700

acc cta ggc aaa gag aca gct cca ccc aca gaa aca aat ttg ggc atg
 Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met
 705 710 715 720

gcc aaa gac atg tct cca ctc cca gaa tca gaa gtg act ctg ggc aag
 Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys
 725 730 735

gac gtg gtt ata ctt cca gaa aca aag gtg gct gag ttt aac aat gtg
 Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val
 740 745 750

act cca ctt tca gaa gaa gag gta acc tca gtc aag gac atg tct ccg
 Thr Pro Leu Ser Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro
 755 760 765

tct gca gaa aca gag gct ccc ctg gct aag aat gct gat ctg cac tca
 Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser
 2352

770	775	780	
gga aca gag ctg att gtg gac aac agc atg gct cca gcc tcc gat ctt Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu 785	790	795	2400
gca ctg ccc ttg gaa aca aaa gta gca aca gtt cca att aaa gac aaa Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys 805	810	815	2448
gga atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 820	825	830	2496
ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser 835	840	845	2544
ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe 850	855	860	2592
atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 865	870	875	2640
acc ctg acc cac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg Thr Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met 885	890	895	2688
aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 900	905	910	2736
gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 915	920	925	2784
gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 930	935	940	2832
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu 945	950	955	2880
tac aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag Tyr Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys 965	970	975	2928
aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly 980	985	990	2976
agc gtg cag ctc gcc gac cac tac cag aac acc ccc atc ggc gac Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 995	1000	1005	3024
ggc ccc gtg ctg ctc gac cac tac ctc gac aac cac acc ccc atc ggc gac Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala 1010	1015	1020	3072

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 3120
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 1025 1030 1035 1040

tcc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 3168
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1045 1050 1055

tag 3171

<210> 32
 <211> 1056
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 NLS-EYFP-MAPKDM-EBFP construct

<400> 32

Met Arg Pro Arg Arg Lys Val Ser Lys Gly Glu Glu Leu Phe Thr Gly
 1 5 10 15

Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 20 25 30

Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 35 40 45

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 50 55 60

Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr
 65 70 75 80

Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
 85 90 95

Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 100 105 110

Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 115 120 125

Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 130 135 140

His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 145 150 155 160

Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
 165 170 175

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 180 185 190

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 195 200 205

Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 210 215 220
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 225 230 235 240
 Glu Leu Tyr Lys Lys Gly Asp Glu Val Asp Gly Ala Asp Leu Ser Leu
 245 250 255
 Val Asp Ala Leu Thr Glu Pro Pro Glu Ile Glu Gly Glu Ile Lys
 260 265 270
 Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val
 275 280 285
 Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp
 290 295 300
 Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Pro Cys Leu Asp Thr
 305 310 315 320
 Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn
 325 330 335
 Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp
 340 345 350
 Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn
 355 360 365
 Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp
 370 375 380
 Thr Asp Gln Ala Glu Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala
 385 390 395 400
 Asp Leu Leu Phe Val Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr
 405 410 415
 Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp
 420 425 430
 Ser Phe Ala Ser Thr Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala
 435 440 445
 Pro Asn Ser Pro Cys Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile
 450 455 460
 Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu
 465 470 475 480
 Ser Val Lys Glu Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu
 485 490 495
 Gln Thr Thr Asp Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly
 500 505 510
 Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys
 515 520 525
 Pro Asp Val Ile Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp

530	535	540
Met Phe Leu Ala Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala		
545	550	555
His Ala Asn Asn Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr		
565	570	575
Lys Asp Val Ala Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp		
580	585	590
Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp		
595	600	605
Leu Ala Pro Pro Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala		
610	615	620
Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala		
625	630	635
Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val		
645	650	655
Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser		
660	665	670
Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala		
675	680	685
Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met		
690	695	700
Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met		
705	710	715
Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys		
725	730	735
Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val		
740	745	750
Thr Pro Leu Ser Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro		
755	760	765
Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser		
770	775	780
Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu		
785	790	795
Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys		
805	810	815
Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile		
820	825	830
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser		
835	840	845
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe		
850	855	860

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 865 870 875 880

Thr Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 885 890 895

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 900 905 910

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 915 920 925

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 930 935 940

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 945 950 955 960

Tyr Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 965 970 975

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 980 985 990

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 995 1000 1005

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 1010 1015 1020

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 1025 1030 1035 1040

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1045 1050 1055

<210> 33
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1623)

<220>
<223> Description of Artificial Sequence:
YFP-NLS-CP3-multiple DEVD-CFP-Annexin II construct

<400> 33
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
35															45		
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	acc	ctc	gtg	acc	acc			192	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50															55	60	
ttc	ggc	tac	ggc	ctg	cag	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240	
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65															70	75	80
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
85															90	95	
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
100															105	110	
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly			
115															120	125	
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
130															135	140	
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145															150	155	160
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc		528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
165															170	175	
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc		576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
180															185	190	
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg		624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu		
195															200	205	
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc		672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe		
210															215	220	
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc		720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser		
225															230	235	240
gga	aga	agg	aaa	cga	caa	aag	cga	tcg	gca	ggt	gac	gaa	gtt	gat	gca		768
Gly	Arg	Arg	Lys	Arg	Gln	Lys	Arg	Ser	Ala	Gly	Asp	Glu	Val	Asp	Ala		
245															250	255	
ggt	gac	gaa	gtt	gat	gca	ggt	gac	gaa	gtt	gat	gca	ggt	gac	gaa	gtt		816
Gly	Asp	Glu	Val	Asp	Ala	Gly	Asp	Glu	Val	Asp	Ala	Gly	Asp	Glu	Val		
260															265	270	
gac	gca	ggt	agt	act	atg	gtg	agc	aag	ggc	gag	gag	ctg	tcc	acc	ggg		864
Asp	Ala	Gly	Ser	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly		

275	280	285	
gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys 290 295 300			912
ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg Phe Ser Val Ser Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu 305 310 315 320			960
acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro 325 330 335			1008
acc ctc gtg acc acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac Thr Leu Val Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr 340 345 350			1056
ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu 355 360 365			1104
ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr 370 375 380			1152
aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg 385 390 395 400			1200
atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly 405 410 415			1248
cac aag ctg gag tac aac tac atc agc cac aac gtc tat atc acc gcc His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala 420 425 430			1296
gac aag cag aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn 435 440 445			1344
atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr 450 455 460			1392
ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser 465 470 475 480			1440
acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met 485 490 495			1488
gtc ctg ctg gag ttc gtg acc gcc ggc ggg atc act ctc ggc atg gac Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp 500 505 510			1536
gag ctg tac aag atg tct act gtc cac gaa atc ctg tgc aag ctc agc Glu Leu Tyr Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser 515 520 525			1584

ttg gag ggt gtt cat tct aca ccc cca agt gcc gga tcc
 Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 530 535 540

<210> 34
 <211> 541
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 YFP-NLS-CP3-multiple DEVD-CFP-Annexin II construct

<400> 34
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240

Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala
 245 250 255
 Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val
 260 265 270
 Asp Ala Gly Ser Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly
 275 280 285
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 290 295 300
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 305 310 315 320
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 325 330 335
 Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr
 340 345 350
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
 355 360 365
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 370 375 380
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 385 390 395 400
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 405 410 415
 His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala
 420 425 430
 Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn
 435 440 445
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
 450 455 460
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 465 470 475 480
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 485 490 495
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 500 505 510
 Glu Leu Tyr Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser
 515 520 525
 Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 530 535 540

 <210> 35
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 35

gactacaaag acgacgcacga caaa

24

<210> 36

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 36

Asp Tyr Lys Asp Asp Asp Asp Lys

1 5

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HA epitope

<400> 37

tacccatacg acgttaccaga ctacgca

27

<210> 38

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HA epitope

<400> 38

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1 5

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: KT3 epitope

<400> 39

ccaccagaac cagaaaca

18

<210> 40

<211> 6

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: KT3 epitope

<400> 40
 Pro Pro Glu Pro Glu Thr
 1 5

<210> 41
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Myc epitope

<400> 41
 gcagaagaac aaaaatata aagcgaagaa gactta

36

<210> 42
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Myc epitope

<400> 42
 Ala Glu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 43
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (717)

<220>
 <223> Description of Artificial Sequence: EYFP

<400> 43
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgcc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg ggc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gtg acc gcc gcc ggg atc act ctc gcc atg gac gag ctg tac aag 717
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 44
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: EYFP

<400> 44
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 45

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(717)

<220>

<223> Description of Artificial Sequence: EGFP

<400> 45

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc			144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag			240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
65	70	75	80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc			576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
180	185	190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg			624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
195	200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc			672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
210	215	220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag			717
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
225	230	235	

<210> 46
<211> 239
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGFP

<400> 46

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1					5				10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
						20			25				30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
					35			40					45		

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Va	Thr	Thr
					50			55			60				

Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
					65			70			75		80		

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
					85			90			95				

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
					100			105			110				

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
					115			120			125				

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
					130			135			140				

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
					145			150			155		160		

Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
					165			170			175				

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asp	Thr	Pro	Ile	Gly	Asp	Gly
					180			185			190				

Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
					195			200			205				

Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
					210			215			220				

Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys
					225			230			235			

<210> 47

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(717)

<220>

<223> Description of Artificial Sequence: EBFP

<400> 47
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc cac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 717
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 48
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: EBFP

<400> 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 49
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(717)

<220>
<223> Description of Artificial Sequence: ECFP

<400> 49

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag
 Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

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aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145          150          155          160

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ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 717
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 50

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ECFP

<400> 50

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

225

230

235

<210> 51
<211> 720
<212> DNA
<213> Art

<220>
<221> CDS
<222> (1) .. (717)

52202

<223> Description of Artificial Sequence: Fred25

<400> 51

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atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 4
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
      1           5           10          15

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gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

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aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145          150          155          160

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gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc qat ggc 576

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tag 720
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 225 230 235

<210> 52

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fred25

<400> 52

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
225 230 235

<210> 53

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 53

tggaaacatg acaa

14

<210> 54

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 54

Trp Glu His Asp
1

<210> 55

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: proCaspase-1
substrate recognition sequence

<400> 55

tggtttaaag ac

12

<210> 56

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: proCaspase-1
substrate recognition sequence

<400> 56

Trp Phe Lys Asp

1

<210> 57
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 57
gacgaacacg ac

12

<210> 58
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 58
Asp Glu His Asp
1

<210> 59
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 59
gacgaagttg ac

12

<210> 60
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 60
Asp Glu Val Asp
1

<210> 61
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 61
atagaaacag ac

12

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 62
Ile Glu Thr Asp
1

<210> 63
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 63
tgggtaagag ac

12

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 64
Trp Val Arg Asp
1

<210> 65
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 65
gtagaaaatag ac

12

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 66
Val Glu Ile Asp
1

<210> 67
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 67
gtagaacacg ac

12

<210> 68
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 68
Val Glu His Asp
1

<210> 69
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 69
acagaagtag ac

12

<210> 70
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 70
Thr Glu Val Asp
1

<210> 71
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 71
ataacaaggcag ac

12

<210> 72
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 72
Ile Gln Ala Asp
1

<210> 73
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 73
gtagaaacag ac

12

<210> 74
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 74
Val Glu Thr Asp
1

<210> 75
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 75
ttagaaacag ac

12

<210> 76
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 76
Leu Glu Thr Asp
1

<210> 77
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 77
ttagaacacg ac

12

<210> 78
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 78
Leu Glu His Asp
1

<210> 79
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 79
ttagaacacg ac

12

<210> 80
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 80
Leu Glu His Asp
1

<210> 81
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 81
agccaaaatt ac

12

<210> 82
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 82
Ser Gln Asn Tyr
1

<210> 83
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 83
ccaatatgtac aa

12

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 57
gacgaacacg ac

12

<210> 58
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 58
Asp Glu His Asp
1

<210> 59
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 59
gacgaagtgc ac

12

<210> 60
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 60
Asp Glu Val Asp
1

<210> 61
<211> 12
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 61
atagaaacag ac

12

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 62
Ile Glu Thr Asp
1

<210> 63
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 63
tgggttaagag ac

12

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 64
Trp Val Arg Asp
1

<210> 65
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 65
gtagaaatag ac

12

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 66
Val Glu Ile Asp
1

<210> 67
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 67
gtagaacacg ac

12

<210> 68
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 68
Val Glu His Asp
1

<210> 69
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 69
acagaagtatg ac

12

<210> 70
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 70
Thr Glu Val Asp
1

<210> 71
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 71
atacaaggcag ac

12

<210> 72
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 72
Ile Gln Ala Asp
1

<210> 73
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 73
gttagaaacag ac

12

<210> 74
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 74
Val Glu Thr Asp
1

<210> 75
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 75
ttagaaacag ac

12

<210> 76
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 76
Leu Glu Thr Asp
1

<210> 77
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 77
ttagaacacg ac

12

<210> 78
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 78
Leu Glu His Asp
1

<210> 79
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 79
ttagaacacg ac

12

<210> 80
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 80
Leu Glu His Asp
1

<210> 81
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 81
agccaaaatt ac

12

<210> 82
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 82
Ser Gln Asn Tyr
1

<210> 83
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 83
ccaatagtagc aa

12

<210> 84
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 84
Pro Ile Val Gln
1

<210> 85
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Adenovirus
endopeptidase substrate recognition sequence

<400> 85
atgtttggag ga

12

<210> 86
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Adenovirus
endopeptidase substrate recognition sequence

<400> 86
Met Phe Gly Gly

1

<210> 87
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Adenovirus
endopeptidase substrate recognition sequence

<400> 87
gcaaaaaaaaaaa ga

12

<210> 88
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Adenovirus
endopeptidase substrate recognition sequence

<400> 88
Ala Lys Lys Arg
1

<210> 89
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 89
gtgaaaaatg

9

<210> 90
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 90
Val Lys Met
1

<210> 91
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase substrate recognition sequence

<400> 91
gacgcagaat tc

12

<210> 92
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase substrate recognition sequence

<400> 92
Asp Ala Glu Phe
1

<210> 93
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cathepsin D substrate recognition sequence

<400> 93
aaaccagcat tattc

15

<210> 94
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cathepsin D substrate recognition sequence

<400> 94
Lys Pro Ala Leu Phe
1 5

<210> 95
<211> 9
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 95

ttcagatta

9

<210> 96

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 96

Phe Arg Leu

1

<210> 97

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Matrix
Metalloprotease substrate recognition sequence

<400> 97

ggaccattag gacca

15

<210> 98

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Matrix
Metalloprotease substrate recognition sequence

<400> 98

Gly Pro Leu Gly Pro

1

5

<210> 99

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Granzyme B
substrate recognition sequence

<400> 99
atagaaccag ac

12

<210> 100
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Granzyme B
substrate recognition sequence

<400> 100
Ile Glu Pro Asp
1

<210> 101
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 101
atgcccaga agaagccgac gcccatccag ctgaac

36

<210> 102
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 102
Met Pro Lys Lys Pro Thr Pro Ile Gln Leu Asn
1 5 10

<210> 103
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 103
atgctggccc ggaggaagcc ggtgctgccg gcgctcacca tcaac

45

<210> 104
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 104
Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn
1 5 10 15

<210> 105
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 105
gcctcgcagt ttgaaaca

18

<210> 106
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 106
Ala Ser Gln Phe Glu Thr
1 5

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 107
gcttctcaat ttgaaacg

18

<210> 108
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulism substrate recognition sequence

<400> 108
Ala Ser Gln Phe Glu Thr
1 5

<210> 109
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin A substrate recognition sequence

<400> 109
gccaaccaac gtgcaaca

18

<210> 110
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin A substrate recognition sequence

<400> 110
Ala Asn Gln Arg Ala Thr
1 5

<210> 111
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin B substrate recognition sequence

<400> 111
gcttctcaat ttgaaacg

18

<210> 112
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin B substrate recognition sequence

<400> 112
Ala Ser Gln Phe Glu Thr
1 5

<210> 113
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin C substrate recognition sequence

<400> 113
acgaaaaaaag ctgtgaaa

18

<210> 114
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin C substrate recognition sequence

<400> 114
Thr Lys Lys Ala Val Lys
1 5

<210> 115
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin D substrate recognition sequence

<400> 115
gaccagaagc tctctgag

18

<210> 116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin D substrate recognition sequence

<400> 116

Asp Gln Lys Leu Ser Glu
1 5

<210> 117

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin E substrate recognition sequence

<400> 117

atcgacagga tcatggag

18

<210> 118

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin E substrate recognition sequence

<400> 118

Ile Asp Arg Ile Met Glu
1 5

<210> 119

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin F substrate recognition sequence

<400> 119

agagaccaga agctctct

18

<210> 120

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin F substrate recognition sequence

<400> 120
Arg Asp Gln Lys Leu Ser
1 5

<210> 121
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum neurotoxin G substrate recognition sequence

<400> 121
acgagcgcag ccaagg 18

<210> 122
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum neurotoxin G substrate recognition sequence

<400> 122
Thr Ser Ala Ala Lys Leu
1 5

<210> 123
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Cytoplasm/cytoskeleton target sequence

<400> 123
atgtctactg tccacgaaat cctgtgcaag ctcagttgg agggtgttca ttctacaccc 60
ccaagtgcc 69

<210> 124
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Cytoplasm/cytoskeleton target sequence

<400> 124
Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val
1 5 10 15

His Ser Thr Pro Pro Ser Ala
20

<210> 125
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Inner surface
of plasma membrane target sequence

<400> 125
atgggatgt a cattaaggcgc agaagacaaa gcagcagt aaagaagcaa aatgatagac 60
agaaaacttaa gagaagacgg agaaaaagct gctaga 96

<210> 126
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Inner surface
of plasma membrane target sequence

<400> 126
Met Gly Cys Thr Leu Ser Ala Glu Asp Lys Ala Ala Val Glu Arg Ser
1 5 10 15

Lys Met Ile Asp Arg Asn Leu Arg Glu Asp Gly Glu Lys Ala Ala Arg
20 25 30

<210> 127
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleus target
sequence

<400> 127
agaaggaaac gacaaaag 18

<210> 128

<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleus target sequence

<400> 128

Arg Arg Lys Arg Gln Lys
1 5

<210> 129

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleolus target sequence

<400> 129

agaaaacgta tacgtactta cctcaagtcc tgcaggcgga tgaaaaagaag tggttttgag 60

atgtctcgac ctattccttc ccaccttact

90

<210> 130

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleolus target sequence

<400> 130

Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys Arg
1 5 10 15

Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr
20 25 30

<210> 131

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mitochondria target sequence

<400> 131

atgtccgtcc tgacgcccgt gctgctgcgg ggcttgacag gctcgccccg gcggctccca 60

gtgcccgcgcg ccaagatcca ttcgttg

87

<210> 132
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mitochondria
target sequence

<400> 132
Met Ser Val Leu Thr Pro Leu Leu Leu Arg Gly Leu Thr Gly Ser Ala
1 5 10 15

Arg Arg Leu Pro Val Pro Arg Ala Leu Ile His Ser Leu
20 25

<210> 133
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear
Envelope target sequence

<400> 133
atgagcattg ttttaataat ttttatttgtg gtgattttt taatatgttt tttatattta 60
agcaacagca aagatcccg agtaccaggta gaattaatg 99

<210> 134
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear
Envelope target sequence

<400> 134
Met Ser Ile Val Leu Ile Ile Val Ile Val Val Ile Phe Leu Ile Cys
1 5 10 15

Phe Leu Tyr Leu Ser Asn Ser Lys Asp Pro Arg Val Pro Val Glu Leu
20 25 30

Met

<210> 135
<211> 246

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Golgi target sequence

<400> 135

atgaggcttc gggagccgct cctgagcggc agcgccgcga tgccaggcgc gtccctacag 60
cgggcctgcc gcctgtcggt ggccgtctgc gctctgcacc ttggcgtaac cctcgtttac 120
tacctggctg gccgcgacct gagccgcctg ccccaactgg tcggagtctc cacacccgtg 180
cagggcggct cgaacagtgc cgccgcctac gggcagtcct ccggggagct ccggaccgga 240
ggggcc

246

<210> 136

<211> 82

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Golgi target sequence

<400> 136

Met Arg Leu Arg Glu Pro Leu Leu Ser Gly Ser Ala Ala Met Pro Gly
1 5 10 15

Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val Cys Ala Leu
20 25 30

His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg Asp Leu Ser
35 40 45

Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln Gly Gly Ser
50 55 60

Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu Arg Thr Gly
65 70 75 80

Gly Ala

<210> 137

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Endoplasmic reticulum target sequence

<400> 137
gaaacaataa gacctataag aataagaaga ttttcttatt ttacatctac agacagcaaa 60
atggcaattc aattaagatc tccctttcca ttagcattac caggaatgtt agctttattta 120
ggatggtgtt ggtttttcag tagaaaaaaaaa 150

<210> 138
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Endoplasmic
reticulum target sequence

<400> 138
Glu Thr Ile Arg Pro Ile Arg Ile Arg Arg Cys Ser Tyr Phe Thr Ser
1 5 10 15

Thr Asp Ser Lys Met Ala Ile Gln Leu Arg Ser Pro Phe Pro Leu Ala
20 25 30

Leu Pro Gly Met Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg
35 40 45

Lys Lys
50

<210> 139
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 139
gccttgcaga agaagctgga ggagctagag cttgatgag 39

<210> 140
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 140
Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
1 5 10

<210> 141
<211> 1024
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Size exclusion target sequence

<400> 141
gcccacccca gtcttggaa tgcgttgaca gaaccaccc cagaaaattga gggagaaaata 60
aagcgagact tcattggctgc gctggaggca gagccctatg atgacatcgt gggagaaaact 120
gtggagaaaa ctgagtttat tcctctccctg gatggtcatg agaaaaccgg gaactcagag 180
tccaaaaaga aaccctgctt agacacttagc cagggtgaag gtatcccata ttctaaacca 240
acactcctag ccaatggtga tcattggatg gaggggaaata acactgcagg gtctccaact 300
gacttccttg aagagagagt ggactatccg gattatcaga gcagccagaa ctggccagaa 360
gatgcaagct tttgtttcca gcctcagcaa gtgttagata ctgaccaggc tgagcccttt 420
aacgagcacc gtgatgatgg tttggcagat ctgcttttg tctccagtgg acccacgaac 480
gcttctgcattt acatggatcg agacaatcc tcagaagaca gttacggat gcttccctgt 540
gactcatttg cttccacggc tggatgtatct caggagtgg ctgtgggagc cccaaactct 600
ccatgttcag agtcctgtgt ctccccagag gttactatag aaaccctaca gccagcaaca 660
gagctctcca aggcagcaga agtggaatca gtgaaagagc agctgccagc taaagcattg 720
gaaacgatgg cagagcagac cactgatgtg gtgcactctc catccacaga cacaacacca 780
ggcccgacaca cagaggcagc actggctaaa gacatagaag agatcaccaa gccagatgtg 840
atattggcaa atgtcacgca gccatctact gaatcgata tggatggc ccaggacatg 900
gaactactca caggaacaga ggcagccac gctaacaata tcatttgcc tacagaacca 960
gacgaatctt caaccaagga tggatgcacca cctatggaaag aagaaaattgt cccaggcaat 1020
gata

1024

<210> 142
<211> 566
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Size exclusion target sequence

<400> 142
 Ala Asp Leu Ser Leu Val Asp Ala Leu Thr Glu Pro Pro Pro Glu Ile
 1 5 10 15
 Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro
 20 25 30
 Tyr Asp Asp Ile Val Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro
 35 40 45
 Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Lys
 50 55 60
 Pro Cys Leu Asp Thr Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro
 65 70 75 80
 Thr Leu Leu Ala Asn Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala
 85 90 95
 Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr
 100 105 110
 Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro
 115 120 125
 Gln Gln Val Leu Asp Thr Asp Gln Ala Glu Pro Phe Asn Glu His Arg
 130 135 140
 Asp Asp Gly Leu Ala Asp Leu Leu Phe Val Ser Ser Gly Pro Thr Asn
 145 150 155 160
 Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr Gly
 165 170 175
 Met Leu Pro Cys Asp Ser Phe Ala Ser Thr Ala Val Val Ser Gln Glu
 180 185 190
 Trp Ser Val Gly Ala Pro Asn Ser Pro Cys Ser Glu Ser Cys Val Ser
 195 200 205
 Pro Glu Val Thr Ile Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser Lys
 210 215 220
 Ala Ala Glu Val Glu Ser Val Lys Glu Gln Leu Pro Ala Lys Ala Leu
 225 230 235 240
 Glu Thr Met Ala Glu Gln Thr Thr Asp Val Val His Ser Pro Ser Thr
 245 250 255
 Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp Ile
 260 265 270
 Glu Glu Ile Thr Lys Pro Asp Val Ile Leu Ala Asn Val Thr Gln Pro
 275 280 285
 Ser Thr Glu Ser Asp Met Phe Leu Ala Gln Asp Met Glu Leu Leu Thr
 290 295 300

Gly Thr Glu Ala Ala His Ala Asn Asn Ile Ile Leu Pro Thr Glu Pro
 305 310 315 320

 Asp Glu Ser Ser Thr Lys Asp Val Ala Pro Pro Met Glu Glu Glu Ile
 325 330 335

 Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr Leu
 340 345 350

 Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr Lys
 355 360 365

 Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile
 370 375 380

 Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val
 385 390 395 400

 Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu
 405 410 415

 Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr
 420 425 430

 Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser
 435 440 445

 Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu
 450 455 460

 Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu
 465 470 475 480

 Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala
 485 490 495

 Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Glu Val Thr Ser Val
 500 505 510

 Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn
 515 520 525

 Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala
 530 535 540

 Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val
 545 550 555 560

 Pro Ile Lys Asp Lys Gly
 565

<210> 143
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 143

atgtgggcaa tcgggattac tggctgggtt atcttcata tcatacatcat cgtgtgggtt 60

gtc

63

<210> 144

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 144

Met Trp Ala Ile Gly Ile Thr Val Leu Val Ile Phe Ile Ile Ile Ile
1 5 10 15Ile Val Trp Val Val
20

<210> 145

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 145

atgtgggcga tagggatcg tagccctggtg atcattgtca tcatacatcat cgtgtggtgt 60

g

61

<210> 146

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 146

Met Trp Ala Ile Gly Ile Ser Val Leu Val Ile Ile Val Ile Ile Ile
1 5 10 15

Ile Val Trp Cys

20

<210> 147

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 147

gacctgcaga agaagctgga ggagctggaa cttgacgag

39

<210> 148

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 148

Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
1 5 10

<210> 149

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peroxisome
target sequence

<400> 149

tctaaaactg

9

<210> 150

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peroxisome
target sequence

<400> 150

Ser Lys Leu

1

<210> 151
 <211> 3378
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(3375)

<400> 151

atg	gcc	gac	ctc	agt	ctt	gtg	gat	gcg	ttg	aca	gaa	cca	cct	cca	gaa	48
Met	Ala	Asp	Leu	Ser	Leu	Val	Asp	Ala	Leu	Thr	Glu	Pro	Pro	Pro	Glu	
1	5					10				15						

att gag gga gaa ata aag cga gac ttc atg gct gcg ctg gag gca gag 96

Ile	Glu	Gly	Glu	Ile	Lys	Arg	Asp	Phe	Met	Ala	Ala	Leu	Glu	Ala	Glu	96
20	25									30						

ccc tat gat gac atc gtg gga gaa act gtg gag aaa act gag ttt att 144

Pro	Tyr	Asp	Asp	Ile	Val	Gly	Glu	Thr	Val	Glu	Lys	Thr	Glu	Phe	Ile	144
35										40						

cct ctc ctg gat ggt gat gag aaa acc ggg aac tca gag tcc aaa aag 192

Pro	Leu	Leu	Asp	Gly	Asp	Glu	Lys	Thr	Gly	Asn	Ser	Glu	Ser	Lys	Lys	192
50										60						

aaa ccc tgc tta gac act agc cag gtt gaa ggt atc cca tct tct aaa 240

Lys	Pro	Cys	Leu	Asp	Thr	Ser	Gln	Val	Glu	Gly	Ile	Pro	Ser	Ser	Lys	240
65										75						

cca aca ctc cta gcc aat ggt gat cat gga atg gag ggg aat aac act 288

Pro	Thr	Leu	Leu	Ala	Asn	Gly	Asp	His	Gly	Met	Glu	Gly	Asn	Asn	Thr	288
85										90						

gca ggg tct cca act gac ttc ctt gaa gag aga gtg gac tat ccg gat 336

Ala	Gly	Ser	Pro	Thr	Asp	Phe	Leu	Glu	Glu	Arg	Val	Asp	Tyr	Pro	Asp	336
100										105			110			

tat cag agc agc cag aac tgg cca gaa gat gca agc ttt tgt ttc cag 384

Tyr	Gln	Ser	Ser	Gln	Asn	Trp	Pro	Glu	Asp	Ala	Ser	Phe	Cys	Phe	Gln	384
115										120			125			

cct cag caa gtg tta gat act gac cag gct gag ccc ttt aac gag cac 432

Pro	Gln	Gln	Val	Leu	Asp	Thr	Asp	Gln	Ala	Glu	Pro	Phe	Asn	Glu	His	432
130										135			140			

cgt gat gat ggt ttg gca gat ctg ctc ttt gtc tcc agt gga ccc acg 480

Arg	Asp	Asp	Gly	Leu	Ala	Asp	Leu	Leu	Phe	Val	Ser	Ser	Gly	Pro	Thr	480
145										150			155			

aac gct tct gca ttt aca gag cga gac aat cct tca gaa gac agt tac 528

Asn	Ala	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Asn	Pro	Ser	Glu	Asp	Ser	Tyr	528
165										170			175			

ggt atg ctt ccc tgt gac tca ttt gct tcc acg gct gtt gta tct cag 576

Gly	Met	Leu	Pro	Cys	Asp	Ser	Phe	Ala	Ser	Thr	Ala	Val	Val	Ser	Gln	576
180										185			190			

gag tgg tct gtg gga gcc cca aac tct cca tgt tca gag tcc tgt gtc Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys Ser Glu Ser Cys Val 195 200 205	624
tcc cca gag gtt act ata gaa acc cta cag cca gca aca gag ctc tcc Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser 210 215 220	672
aag gca gca gaa gtg gaa tca gtg aaa gag cag ctg cca gct aaa gca Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln Leu Pro Ala Lys Ala 225 230 235 240	720
ttg gaa acg atg gca gag cag acc act gat gtg gtg cac tct cca tcc Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val Val His Ser Pro Ser 245 250 255	768
aca gac aca aca cca ggc cca gac aca gag gca gca ctg gct aaa gac Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp 260 265 270	816
ata gaa gag atc acc aag cca gat gtg ata ttg gca aat gtc acg cag Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu Ala Asn Val Thr Gln 275 280 285	864
cca tct act gaa tcg gat atg ttc ctg gcc cag gac atg gaa cta ctc Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln Asp Met Glu Leu Leu 290 295 300	912
aca gga aca gag gca gcc cac gct aac aat atc ata ttg cct aca gaa Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile Ile Leu Pro Thr Glu 305 310 315 320	960
cca gac gaa tct tca acc aag gat gta gca cca cct atg gaa gaa gaa Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro Pro Met Glu Glu Glu 325 330 335	1008
att gtc cca ggc aat gat acg aca tcc ccc aaa gaa aca gag aca aca Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr 340 345 350	1056
ctt cca ata aaa atg gac ttg gca cca cct gag gat gtg tta ctt acc Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr 355 360 365	1104
aaa gaa aca gaa cta gcc cca gcc aag ggc atg gtt tca ctc tca gaa Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu 370 375 380	1152
ata gaa gag gct ctg gca aag aat gat gtt cgc tct gca gaa ata cct Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro 385 390 395 400	1200
gtg gct cag gag aca gtg gtc tca gaa aca gag gtg gtc ctg gca aca Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr 405 410 415	1248

gaa gtg gta ctg ccc tca gat ccc ata aca aca ttg aca aag gat gtg 1296
 Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val
 420 425 430

 aca ctc ccc tta gaa gca gag aga ccg ttg gtg acg gac atg act cca 1344
 Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro
 435 440 445

 tct ctg gaa aca gaa atg acc cta ggc aaa gag aca gct cca ccc aca 1392
 Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr
 450 455 460

 gaa aca aat ttg ggc atg gcc aaa gac atg tct cca ctc cca gaa tca 1440
 Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser
 465 470 475 480

 gaa gtg act ctg ggc aag gac gtg gtt ata ctt cca gaa aca aag gtg 1488
 Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val
 485 490 495

 gct gag ttt aac aat gtg act cca ctt tca gaa gaa gag gta acc tca 1536
 Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Val Thr Ser
 500 505 510

 gtc aag gac atg tct ccg tct gca gaa aca gag gct ccc ctg gct aag 1584
 Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys
 515 520 525

 aat gct gat ctg cac tca gga aca gag ctg att gtg gac aac agc atg 1632
 Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met
 530 535 540

 gct cca gcc tcc gat ctt gca ctg ccc ttg gaa aca aaa gta gca aca 1680
 Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr
 545 550 555 560

 gtt cca att aaa gac aaa gga act gta cag act gaa gaa aaa cca cgt 1728
 Val Pro Ile Lys Asp Lys Gly Thr Val Gln Thr Glu Glu Lys Pro Arg
 565 570 575

 gaa gac tcc cag tta gca tct atg cag cac aag gga cag tca aca gta 1776
 Glu Asp Ser Gln Leu Ala Ser Met Gln His Lys Gly Gln Ser Thr Val
 580 585 590

 cct cct tgc acg gct tca cca gaa cca gtc aaa gct gca gaa caa atg 1824
 Pro Pro Cys Thr Ala Ser Pro Glu Pro Val Lys Ala Ala Glu Gln Met
 595 600 605

 tct acc tta cca ata gat gca cct tct cca tta gag aac tta gag cag 1872
 Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro Leu Glu Asn Leu Glu Gln
 610 615 620

 aag gaa acg cct ggc agc cag cct tct gag cct tgc tca gga gta tcc 1920
 Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu Pro Cys Ser Gly Val Ser
 625 630 635 640

 cgg caa gaa gaa gca aag gct gct gta ggt gtg act gga aat gac atc 1968

Arg Gln Glu Glu Ala Lys Ala Ala Val Gly Val Thr Gly Asn Asp Ile			
645	650	655	
act acc ccg cca aac aag gag cca cca agc cca gaa aag aaa gca		2016	
Thr Thr Pro Pro Asn Lys Glu Pro Pro Ser Pro Glu Lys Lys Ala			
660	665	670	
aag cct ttg gcc acc actcaa cct gca aag act tca aca tcg aaa gcc		2064	
Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys Thr Ser Thr Ser Lys Ala			
675	680	685	
aaa aca cag ccc act tct ctc cct aag caa cca gct ccc acc acc tct		2112	
Lys Thr Gln Pro Thr Ser Leu Pro Lys Gln Pro Ala Pro Thr Thr Ser			
690	695	700	
ggg ggg ttg aat aaa aaa ccc atg agc ctc gcc tca ggc tca gtg cca		2160	
Gly Gly Leu Asn Lys Lys Pro Met Ser Leu Ala Ser Gly Ser Val Pro			
705	710	715	720
gct gcc cca cac aaa cgc cct gct gct gcc act gct act gcc agg cct		2208	
Ala Ala Pro His Lys Arg Pro Ala Ala Ala Thr Ala Thr Ala Arg Pro			
725	730	735	
tcc acc cta cct gcc aga gac gtg aag cca aag cca att aca gaa gct		2256	
Ser Thr Leu Pro Ala Arg Asp Val Lys Pro Lys Pro Ile Thr Glu Ala			
740	745	750	
aag gtt gcc gaa aag cgg acc tct cca tcc aag cct tca tct gcc cca		2304	
Lys Val Ala Glu Lys Arg Thr Ser Pro Ser Lys Pro Ser Ser Ala Pro			
755	760	765	
gcc ctc aaa cct gga cct aaa acc acc cca acc gtt tca aaa gcc aca		2352	
Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro Thr Val Ser Lys Ala Thr			
770	775	780	
tct ccc tca act ctt gtt tcc act gga cca agt agt aga agt cca gct		2400	
Ser Pro Ser Thr Leu Val Ser Thr Gly Pro Ser Ser Arg Ser Pro Ala			
785	790	795	800
aca act ctg cct aag agg cca acc agc atc aag act gag ggg aaa cct		2448	
Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile Lys Thr Glu Gly Lys Pro			
805	810	815	
gct gat gtc aaa agg atg act gct aag tct gcc tca gct gac ttg agt		2496	
Ala Asp Val Lys Arg Met Thr Ala Lys Ser Ala Ser Ala Asp Leu Ser			
820	825	830	
cgc tca aag acc acc tct gcc agt tct gtg aag aga aac acc act ccc		2544	
Arg Ser Lys Thr Thr Ser Ala Ser Ser Val Lys Arg Asn Thr Thr Pro			
835	840	845	
act ggg gca gca ccc cca gca ggg atg act tcc act cga gtc aag ccc		2592	
Thr Gly Ala Ala Pro Pro Ala Gly Met Thr Ser Thr Arg Val Lys Pro			
850	855	860	
atg tct gca cct agc cgc tct tct ggg gct ctt tct gtg gac aag aag		2640	
Met Ser Ala Pro Ser Arg Ser Ser Gly Ala Leu Ser Val Asp Lys Lys			

865	870	875	880	
ccc act tcc act aag cct agc tcc tct gct ccc agg gtg agc cgc ctg Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala Pro Arg Val Ser Arg Leu				2688
885	890	895		
gcc aca act gtt tct gcc cct gac ctg aag agt gtt cgc tcc aag gtc Ala Thr Thr Val Ser Ala Pro Asp Leu Lys Ser Val Arg Ser Lys Val				2736
900	905	910		
ggc tct aca gaa aac atc aaa cac cag cct gga gga ggc cgg gcc aaa Gly Ser Thr Glu Asn Ile Lys His Gln Pro Gly Gly Arg Ala Lys				2784
915	920	925		
gta gag aaa aaa aca gag gca gct acc aca gct ggg aag cct gaa cct Val Glu Lys Lys Thr Glu Ala Ala Thr Thr Ala Gly Lys Pro Glu Pro				2832
930	935	940		
aat gca gtc act aaa gca gcc ggc tcc att gcg agt gca cag aaa ccg Asn Ala Val Thr Lys Ala Ala Gly Ser Ile Ala Ser Ala Gln Lys Pro				2880
945	950	955	960	
cct gct ggg aaa gtc cag ata gta tcc aaa aaa gtg agc tac agt cat Pro Ala Gly Lys Val Gln Ile Val Ser Lys Lys Val Ser Tyr Ser His				2928
965	970	975		
att caa tcc aag tgt gtt tcc aag gac aat att aag cat gtc cct gga Ile Gln Ser Lys Cys Val Ser Lys Asp Asn Ile Lys His Val Pro Gly				2976
980	985	990		
tgt ggc aat gtt cag att cag aac aag aaa gtg gac ata tcc aag gtc Cys Gly Asn Val Gln Ile Gln Asn Lys Lys Val Asp Ile Ser Lys Val				3024
995	1000	1005		
tcc tcc aag tgt ggg tcc aaa gct aat atc aag cac aag cct ggt gga Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile Lys His Lys Pro Gly Gly				3072
1010	1015	1020		
gga gat gtc aag att gaa agt cag aag ttg aac ttc aag gag aag gcc Gly Asp Val Lys Ile Glu Ser Gln Lys Leu Asn Phe Lys Glu Lys Ala				3120
1025	1030	1035	1040	
caa gcc aaa gtg gga tcc ctt gat aac gtt ggc cac ttt cct gca gga Gln Ala Lys Val Gly Ser Leu Asp Asn Val Gly His Phe Pro Ala Gly				3168
1045	1050	1055		
ggt gcc gtg aag act gag ggc ggt ggc agt gag gcc ctt ccg tgt cca Gly Ala Val Lys Thr Glu Gly Gly Ser Glu Ala Leu Pro Cys Pro				3216
1060	1065	1070		
ggc ccc ccc gct ggg gag gag cca gtc atc cct gag gct gcg cct gac Gly Pro Pro Ala Gly Glu Pro Val Ile Pro Glu Ala Ala Pro Asp				3264
1075	1080	1085		
cgt ggc gcc cct act tca gcc agt ggc ctc agt ggc cac acc acc ctg Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu Ser Gly His Thr Thr Leu				3312
1090	1095	1100		

tca	ggg	ggt	ggt	gac	caa	agg	gag	ccc	cag	acc	ttg	gac	agc	cag	atc	3360
Ser	Gly	Gly	Gly	Asp	Gln	Arg	Glu	Pro	Gln	Thr	Leu	Asp	Ser	Gln	Ile	
1105															1120	
cag gag aca agc atc taa															3378	
Gln Glu Thr Ser Ile																
1125																
<210> 152																
<211> 1125																
<212> PRT																
<213> Mus musculus																
<400> 152																
Met	Ala	Asp	Leu	Ser	Leu	Val	Asp	Ala	Leu	Thr	Glu	Pro	Pro	Pro	Glu	
1															15	
Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu																
20 25 30																
Pro	Tyr	Asp	Asp	Ile	Val	Gly	Glu	Thr	Val	Glu	Lys	Thr	Glu	Phe	Ile	
35															45	
Pro	Leu	Leu	Asp	Gly	Asp	Glu	Lys	Thr	Gly	Asn	Ser	Glu	Ser	Lys	Lys	
50															60	
Lys	Pro	Cys	Leu	Asp	Thr	Ser	Gln	Val	Glu	Gly	Ile	Pro	Ser	Ser	Lys	
65															80	
Pro	Thr	Leu	Leu	Ala	Asn	Gly	Asp	His	Gly	Met	Glu	Gly	Asn	Asn	Thr	
85															95	
Ala	Gly	Ser	Pro	Thr	Asp	Phe	Leu	Glu	Glu	Arg	Val	Asp	Tyr	Pro	Asp	
100															110	
Tyr	Gln	Ser	Ser	Gln	Asn	Trp	Pro	Glu	Asp	Ala	Ser	Phe	Cys	Phe	Gln	
115															125	
Pro	Gln	Gln	Val	Leu	Asp	Thr	Asp	Gln	Ala	Glu	Pro	Phe	Asn	Glu	His	
130															140	
Arg	Asp	Asp	Gly	Leu	Ala	Asp	Leu	Leu	Phe	Val	Ser	Ser	Gly	Pro	Thr	
145															160	
Asn	Ala	Ser	Ala	Phe	Thr	Glu	Arg	Asp	Asn	Pro	Ser	Glu	Asp	Ser	Tyr	
165															175	
Gly	Met	Leu	Pro	Cys	Asp	Ser	Phe	Ala	Ser	Thr	Ala	Val	Val	Ser	Gln	
180															190	
Glu	Trp	Ser	Val	Gly	Ala	Pro	Asn	Ser	Pro	Cys	Ser	Glu	Ser	Cys	Val	
195															205	
Ser	Pro	Glu	Val	Thr	Ile	Glu	Thr	Leu	Gln	Pro	Ala	Thr	Glu	Leu	Ser	
210															220	

Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln Leu Pro Ala Lys Ala
 225 230 235 240

 Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val Val His Ser Pro Ser
 245 250 255

 Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp
 260 265 270

 Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu Ala Asn Val Thr Gln
 275 280 285

 Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln Asp Met Glu Leu Leu
 290 295 300

 Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile Ile Leu Pro Thr Glu
 305 310 315 320

 Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro Pro Met Glu Glu Glu
 325 330 335

 Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr
 340 345 350

 Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr
 355 360 365

 Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu
 370 375 380

 Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro
 385 390 395 400

 Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr
 405 410 415

 Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val
 420 425 430

 Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro
 435 440 445

 Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr
 450 455 460

 Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser
 465 470 475 480

 Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val
 485 490 495

 Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Glu Val Thr Ser
 500 505 510

 Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys
 515 520 525

Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met
530 535 540

Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr
545 550 555 560

Val Pro Ile Lys Asp Lys Gly Thr Val Gln Thr Glu Glu Lys Pro Arg
565 570 575

Glu Asp Ser Gln Leu Ala Ser Met Gln His Lys Gly Gln Ser Thr Val
580 585 590

Pro Pro Cys Thr Ala Ser Pro Glu Pro Val Lys Ala Ala Glu Gln Met
595 600 605

Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro Leu Glu Asn Leu Glu Gln
610 615 620

Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu Pro Cys Ser Gly Val Ser
625 630 635 640

Arg Gln Glu Glu Ala Lys Ala Ala Val Gly Val Thr Gly Asn Asp Ile
645 650 655

Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro Ser Pro Glu Lys Lys Ala
660 665 670

Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys Thr Ser Thr Ser Lys Ala
675 680 685

Lys Thr Gln Pro Thr Ser Leu Pro Lys Gln Pro Ala Pro Thr Thr Ser
690 695 700

Gly Gly Leu Asn Lys Lys Pro Met Ser Leu Ala Ser Gly Ser Val Pro
705 710 715 720

Ala Ala Pro His Lys Arg Pro Ala Ala Ala Thr Ala Thr Ala Arg Pro
725 730 735

Ser Thr Leu Pro Ala Arg Asp Val Lys Pro Lys Pro Ile Thr Glu Ala
740 745 750

Lys Val Ala Glu Lys Arg Thr Ser Pro Ser Lys Pro Ser Ser Ala Pro
755 760 765

Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro Thr Val Ser Lys Ala Thr
770 775 780

Ser Pro Ser Thr Leu Val Ser Thr Gly Pro Ser Ser Arg Ser Pro Ala
785 790 795 800

Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile Lys Thr Glu Gly Lys Pro
805 810 815

Ala Asp Val Lys Arg Met Thr Ala Lys Ser Ala Ser Ala Asp Leu Ser
820 825 830

Arg Ser Lys Thr Thr Ser Ala Ser Ser Val Lys Arg Asn Thr Thr Pro
835 840 845

Thr Gly Ala Ala Pro Pro Ala Gly Met Thr Ser Thr Arg Val Lys Pro
850 855 860

Met Ser Ala Pro Ser Arg Ser Ser Gly Ala Leu Ser Val Asp Lys Lys
865 870 875 880

Pro Thr Ser Thr Lys Pro Ser Ser Ala Pro Arg Val Ser Arg Leu
885 890 895

Ala Thr Thr Val Ser Ala Pro Asp Leu Lys Ser Val Arg Ser Lys Val
900 905 910

Gly Ser Thr Glu Asn Ile Lys His Gln Pro Gly Gly Gly Arg Ala Lys
915 920 925

Val Glu Lys Lys Thr Glu Ala Ala Thr Thr Ala Gly Lys Pro Glu Pro
930 935 940

Asn Ala Val Thr Lys Ala Ala Gly Ser Ile Ala Ser Ala Gln Lys Pro
945 950 955 960

Pro Ala Gly Lys Val Gln Ile Val Ser Lys Lys Val Ser Tyr Ser His
965 970 975

Ile Gln Ser Lys Cys Val Ser Lys Asp Asn Ile Lys His Val Pro Gly
980 985 990

Cys Gly Asn Val Gln Ile Gln Asn Lys Lys Val Asp Ile Ser Lys Val
995 1000 1005

Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile Lys His Lys Pro Gly Gly
1010 1015 1020

Gly Asp Val Lys Ile Glu Ser Gln Lys Leu Asn Phe Lys Glu Lys Ala
1025 1030 1035 1040

Gln Ala Lys Val Gly Ser Leu Asp Asn Val Gly His Phe Pro Ala Gly
1045 1050 1055

Gly Ala Val Lys Thr Glu Gly Gly Ser Glu Ala Leu Pro Cys Pro
1060 1065 1070

Gly Pro Pro Ala Gly Glu Glu Pro Val Ile Pro Glu Ala Ala Pro Asp
1075 1080 1085

Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu Ser Gly His Thr Thr Leu
1090 1095 1100

Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln Thr Leu Asp Ser Gln Ile
1105 1110 1115 1120

Gln Glu Thr Ser Ile
1125

<210> 153
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 153
tcatcatccg gagctggagc cggagctggc cgatcggttg ttaaatctga aggaaagaga 60
aagtgtacg aagttgatgg aatttgatgaa gtagca 96

<210> 154
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 154
gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaaagctga gcttgcacag 60
gatttcgtgg acagtagaca tagtacttgc tacttcatc 99

<210> 155
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 155
tcatcatccg gagctgg 18

<210> 156
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 156
gaagaaggat ccggcact 18

<210> 157
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 157
tcatcatccg gaagaaggaa acgacaaaag cgatcggttg ttaaatctga aggaaagaga 60
aagtgtgacg aagttgatgg aattgatgaa gtagca 96

<210> 158
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 158
tcatcatccg gaagaagg 18

<210> 159
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 159
tcatcatccg gaagaaggaa acgacaaaag cgatcgacaa gacttggta aattgacaac 60

<210> 160
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 160
gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
gatttcgtgg acagtagaca tagtactgtt gtcaatttc 99

<210> 161
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 161
tcatcatccg gaagaaggaa acgacaaaag cgatcgatc aaaaaggaat accagttgaa 60
acagacagcg aagagcaacc ttat 84

<210> 162
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 162
gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
gatttcgtgg acagtagaca tagtactata agtttgctc 99

<210> 163
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 163
tcatcatccc gaagaaaaacg tatacgtaact tacctaagt cctgcaggcg gatgaaaaga 60

<210> 164
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 164
gaagaacgat cgagtaagggt gggaaaggaat aggtcgagac atctcaaaac cacttcttt 60
cat 63

<210> 165
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 165
tcatcatccg gaagaaaa

18

<210> 166
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 166
gaagaacgtat cgagtaag

18

<210> 167
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 167
ttagaacatg acaa

14

<210> 168
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 168
Leu Glu His Asp
1

<210> 169
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP-HSP27

<220>

<221> CDS

<222> (1)..(1380)

<400> 169

atg	gtg	agc	aag	ggc	gag	gag	ctg	tcc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1	5							10				15					

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	tcc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
20	25							30									

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	tcc	agc	gtg	tcc	ggc		144
Glu	Gly	Gly	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
35	40							45								

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Lys	Phe	Ile		
50	55							60									

ctg	acc	acc	ggc	gtg	cag	tgc	tcc	agc	cgc	tac	ccc	gac	cac	atg	aag		240
Leu	Thr	Thr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
65	70							75				80					

cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
85	90							95									

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
100	105							110									

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
115	120							125									

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
130	135							140									

aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145	150							155				160					

ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc		528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
165	170							175									

gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc		576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
180	185							190									

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
gga ctc aga tct cga gcg gcg tcc aga gca gag tca gcc agc atg acc	768
Gly Leu Arg Ser Arg Ala Ala Ser Arg Ala Glu Ser Ala Ser Met Thr	
245 250 255	
gag cgc cgc gtc ccc ttc tcg ctc ctg cgg ggc ccc agc tgg gac ccc	816
Glu Arg Arg Val Pro Phe Ser Leu Leu Arg Gly Pro Ser Trp Asp Pro	
260 265 270	
ttc cgc gac tgg tac ccg cat agc cgc ctc ttc gac cag gcc ttc ggg	864
Phe Arg Asp Trp Tyr Pro His Ser Arg Leu Phe Asp Gln Ala Phe Gly	
275 280 285	
ctg ccc cgg ctg ccc gag gag tgg tcg cag tgg tta ggc ggc agc agc	912
Leu Pro Arg Leu Pro Glu Glu Trp Ser Gln Trp Leu Gly Gly Ser Ser	
290 295 300	
tgg cca ggc tac gtg cgc ccc ctg ccc ccc gcc atc gag agc ccc	960
Trp Pro Gly Tyr Val Arg Pro Leu Pro Pro Ala Ala Ile Glu Ser Pro	
305 310 315 320	
gca gtg gcc gcg ccc gcc tac agc cgc gcg ctc agc cgg caa ctc agc	1008
Ala Val Ala Ala Pro Ala Tyr Ser Arg Ala Leu Ser Arg Gln Leu Ser	
325 330 335	
agc ggg gtc tcg gag atc cgg cac act gcg gac cgc tgg cgc gtg tcc	1056
Ser Gly Val Ser Glu Ile Arg His Thr Ala Asp Arg Trp Arg Val Ser	
340 345 350	
ctg gat gtc aac cac ttc gcc ccc gag ctg acg gtc aag acc aag	1104
Leu Asp Val Asn His Phe Ala Pro Asp Glu Leu Thr Val Lys Thr Lys	
355 360 365	
gat ggc gtg gtg gag atc acc ggc aag cac gag gag cgg cag gac gag	1152
Asp Gly Val Val Glu Ile Thr Gly Lys His Glu Glu Arg Gln Asp Glu	
370 375 380	
cat ggc tac atc tcc cgg tgc ttc acg cgg aaa tac acg ctg ccc ccc	1200
His Gly Tyr Ile Ser Arg Cys Phe Thr Arg Lys Tyr Thr Leu Pro Pro	
385 390 395 400	
ggt gtg gac ccc acc caa gtt tcc tcc ctg tcc cct gag ggc aca	1248
Gly Val Asp Pro Thr Gln Val Ser Ser Leu Ser Pro Glu Gly Thr	
405 410 415	
ctg acc gtg gag gcc ccc atg ccc aag cta gcc acg cag tcc aac gag	1296

Leu Thr Val Glu Ala Pro Met Pro Lys Leu Ala Thr Gln Ser Asn Glu
 420 425 430

 atc acc atc cca gtc acc ttc gag tcg cgg gcc cag ctt ggg ggc cca 1344
 Ile Thr Ile Pro Val Thr Phe Glu Ser Arg Ala Gln Leu Gly Gly Pro
 435 440 445

 gaa gct gca aaa tcc gat gag act gcc gcc aag taa 1380
 Glu Ala Ala Lys Ser Asp Glu Thr Ala Ala Lys
 450 455 460

 <210> 170
 <211> 459
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: GFP-HSP27

 <400> 170
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Arg Ala Ala Ser Arg Ala Glu Ser Ala Ser Met Thr
 245 250 255
 Glu Arg Arg Val Pro Phe Ser Leu Leu Arg Gly Pro Ser Trp Asp Pro
 260 265 270
 Phe Arg Asp Trp Tyr Pro His Ser Arg Leu Phe Asp Gln Ala Phe Gly
 275 280 285
 Leu Pro Arg Leu Pro Glu Glu Trp Ser Gln Trp Leu Gly Gly Ser Ser
 290 295 300
 Trp Pro Gly Tyr Val Arg Pro Leu Pro Pro Ala Ala Ile Glu Ser Pro
 305 310 315 320
 Ala Val Ala Ala Pro Ala Tyr Ser Arg Ala Leu Ser Arg Gln Leu Ser
 325 330 335
 Ser Gly Val Ser Glu Ile Arg His Thr Ala Asp Arg Trp Arg Val Ser
 340 345 350
 Leu Asp Val Asn His Phe Ala Pro Asp Glu Leu Thr Val Lys Thr Lys
 355 360 365
 Asp Gly Val Val Glu Ile Thr Gly Lys His Glu Glu Arg Gln Asp Glu
 370 375 380
 His Gly Tyr Ile Ser Arg Cys Phe Thr Arg Lys Tyr Thr Leu Pro Pro
 385 390 395 400
 Gly Val Asp Pro Thr Gln Val Ser Ser Ser Leu Ser Pro Glu Gly Thr
 405 410 415
 Leu Thr Val Glu Ala Pro Met Pro Lys Leu Ala Thr Gln Ser Asn Glu
 420 425 430
 Ile Thr Ile Pro Val Thr Phe Glu Ser Arg Ala Gln Leu Gly Gly Pro
 435 440 445
 Glu Ala Ala Lys Ser Asp Glu Thr Ala Ala Lys
 450 455

<210> 171
 <211> 2823
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP-HSP70

<220>

<221> CDS

<222> (1)...(2823)

<400> 171

atg	gtg	agc	aag	ggc	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1	5															15	

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	tgc	acc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
20	25															30	

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	tgc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
35	40															45	

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50	55															60	

ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag		240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
65	70															80	

cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
85	90															95	

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
100	105															110	

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
115	120															125	

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
130	135															140	

aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145	150															160	

ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc		528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
165	170															175	

gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc		576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
180	185															190	

ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg		624
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
195	200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc			672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
210	215	220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc			720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
225	230	235	240
gga atg tcg gtg ggc ata gac ctg ggc ttc cag agc tgc tac gtc			768
Gly Met Ser Val Val Gly Ile Asp Leu Gly Phe Gln Ser Cys Tyr Val			
245	250	255	
gct gtg gcc cgc gcc ggc ggc atc gag act atc gct aat gag tat agc			816
Ala Val Ala Arg Ala Gly Gly Ile Glu Thr Ile Ala Asn Glu Tyr Ser			
260	265	270	
gac cgc tgc acg ccg gct tgc att tct ttt ggt cct aag aat cgt tca			864
Asp Arg Cys Thr Pro Ala Cys Ile Ser Phe Gly Pro Lys Asn Arg Ser			
275	280	285	
att gga gca gca gct aaa agc cag gta att tct aat gca aag aac aca			912
Ile Gly Ala Ala Ala Lys Ser Gln Val Ile Ser Asn Ala Lys Asn Thr			
290	295	300	
gtc caa gga ttt aaa aga ttc cat ggc cga gca ttc tct gat cca ttt			960
Val Gln Gly Phe Lys Arg Phe His Gly Arg Ala Phe Ser Asp Pro Phe			
305	310	315	320
gtg gag gca gaa aaa tct aac ctt gca tat gat att gtg cag tgg cct			1008
Val Glu Ala Glu Lys Ser Asn Leu Ala Tyr Asp Ile Val Gln Trp Pro			
325	330	335	
aca gga tta aca ggt ata aag gtg aca tat atg gag gaa gag cga aat			1056
Thr Gly Leu Thr Gly Ile Lys Val Thr Tyr Met Glu Glu Arg Asn			
340	345	350	
ttt acc act gagcaa gtg act gcc atg ctt ttg tcc aaa ctg aag gag			1104
Phe Thr Thr Glu Gln Val Thr Ala Met Leu Leu Ser Lys Leu Lys Glu			
355	360	365	
aca gcc gaa agt gtt ctt aag aag cct gta gtt gac tgt gtt gtt tcg			1152
Thr Ala Glu Ser Val Leu Lys Lys Pro Val Val Asp Cys Val Val Ser			
370	375	380	
gtt cct tgt ttc tat act gat gca gaa aga cga tca gtg atg gat gca			1200
Val Pro Cys Phe Tyr Thr Asp Ala Glu Arg Arg Ser Val Met Asp Ala			
385	390	395	400
aca cag att gct ggt ctt aat tgc ttg cga tta atg aat gaa acc act			1248
Thr Gln Ile Ala Gly Leu Asn Cys Leu Arg Leu Met Asn Glu Thr Thr			
405	410	415	
gca gtt gct ctt gca tat gga atc tat aag cag gat ctt cct cgc tta			1296
Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Arg Leu			

420	425	430	
gaa gag aaa cca aga aat gta gtt ttt gta gac atg ggc cac tct gct Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met Gly His Ser Ala 435	440	445	1344
tat caa gtt tct gta tgt gca ttt aat aga gga aaa ctg aaa gtt ctg Tyr Gln Val Ser Val Cys Ala Phe Asn Arg Gly Lys Leu Lys Val Leu 450	455	460	1392
gcc act gca ttt gac acg aca ttg gga ggt aga aaa ttt gat gaa gtg Ala Thr Ala Phe Asp Thr Thr Leu Gly Gly Arg Lys Phe Asp Glu Val 465	470	475	1440
tta gta aat cac ttc tgt gaa gaa ttt ggg aag aaa tac aag cta gac Leu Val Asn His Phe Cys Glu Glu Phe Gly Lys Lys Tyr Lys Leu Asp 485	490	495	1488
att aag tcc aaa atc cgt gca tta tta cga ctc tct cag gag tgt gag Ile Lys Ser Lys Ile Arg Ala Leu Leu Arg Leu Ser Gln Glu Cys Glu 500	505	510	1536
aaa ctc aag aaa ttg atg agt gca aat gct tca gat ctc cct ttg agc Lys Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp Leu Pro Leu Ser 515	520	525	1584
att gaa tgt ttt atg aat gat gtt gat gta tct gga act atg aat aga Ile Glu Cys Phe Met Asn Asp Val Asp Val Ser Gly Thr Met Asn Arg 530	535	540	1632
ggc aaa ttt ctg gag atg tgc aat gat ctc tta gct aga gtg gag cca Gly Lys Phe Leu Glu Met Cys Asn Asp Leu Leu Ala Arg Val Glu Pro 545	550	555	1680
cca ctt cgt agt gtt ttg gaa caa acc aag tta aag aaa gaa gat att Pro Leu Arg Ser Val Leu Glu Gln Thr Lys Leu Lys Lys Glu Asp Ile 565	570	575	1728
tat gca gtg gag ata gtt ggt ggt gct aca cga atc cct gcc gta aaa Tyr Ala Val Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys 580	585	590	1776
gag aag atc agc aaa ttt ttc ggt aaa gaa ctt agt aca aca tta aat Glu Lys Ile Ser Lys Phe Phe Gly Lys Glu Leu Ser Thr Thr Leu Asn 595	600	605	1824
gct gat gaa gct gtc act cga ggc tgt gca ttg cag tgt gcc atc tta Ala Asp Glu Ala Val Thr Arg Gly Cys Ala Leu Gln Cys Ala Ile Leu 610	615	620	1872
tcg cct gct ttc aaa gtc aga gaa ttt tct atc act gat gta gta cca Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Ile Thr Asp Val Val Pro 625	630	635	1920
tat cca ata tct ctg aga tgg aat tct cca gct gaa gaa ggg tca agt Tyr Pro Ile Ser Leu Arg Trp Asn Ser Pro Ala Glu Glu Gly Ser Ser 645	650	655	1968

gac tgt gaa gtc ttt tcc aaa aat cat gct gct cct ttc tct aaa gtt 2016
 Asp Cys Glu Val Phe Ser Lys Asn His Ala Ala Pro Phe Ser Lys Val
 660 665 670

ctt aca ttt tat aga aag gaa cct ttc act ctt gag gcc tac tac agc 2064
 Leu Thr Phe Tyr Arg Lys Glu Pro Phe Thr Leu Glu Ala Tyr Tyr Ser
 675 680 685

tct cct cag gat ttg ccc tat cca gat cct gct ata gct cag ttt tca 2112
 Ser Pro Gln Asp Leu Pro Tyr Pro Asp Pro Ala Ile Ala Gln Phe Ser
 690 695 700

gtt cag aaa gtc act cct cag tct gat ggc tcc agt tca aaa gtg aaa 2160
 Val Gln Lys Val Thr Pro Gln Ser Asp Gly Ser Ser Ser Lys Val Lys
 705 710 715 720

gtc aaa gtt cga gta aat gtc cat ggc att ttc agt gtg tcc agt gca 2208
 Val Lys Val Arg Val Asn Val His Gly Ile Phe Ser Val Ser Ser Ala
 725 730 735

tct tta gtg gag gtt cac aag tct gag gaa aat gag gag cca atg gaa 2256
 Ser Leu Val Glu Val His Lys Ser Glu Glu Asn Glu Glu Pro Met Glu
 740 745 750

aca gat cag aat gca aag gag gaa gag aag atg caa gtg gac cag gag 2304
 Thr Asp Gln Asn Ala Lys Glu Glu Lys Met Gln Val Asp Gln Glu
 755 760 765

gaa cca cat gtt gaa gag caa cag cag cag aca cca gca gaa aat aag 2352
 Glu Pro His Val Glu Glu Gln Gln Gln Thr Pro Ala Glu Asn Lys
 770 775 780

gca gag tct gaa gaa atg gag acc tct caa gct gga tcc aag gat aaa 2400
 Ala Glu Ser Glu Glu Met Glu Thr Ser Gln Ala Gly Ser Lys Asp Lys
 785 790 795 800

aag atg gac caa cca ccc caa tgc caa gaa ggc aaa agt gaa gac cag 2448
 Lys Met Asp Gln Pro Pro Gln Cys Gln Glu Gly Lys Ser Glu Asp Gln
 805 810 815

tac tgt gga cct gcc aat cga gaa tca gct ata tgg cag ata gac aga 2496
 Tyr Cys Gly Pro Ala Asn Arg Glu Ser Ala Ile Trp Gln Ile Asp Arg
 820 825 830

gag atg ctc aac ttg tac att gaa aat gag ggt aag atg atc atg cag 2544
 Glu Met Leu Asn Leu Tyr Ile Glu Asn Glu Gly Lys Met Ile Met Gln
 835 840 845

gat aaa ctg gag aag gag cgg aat gat gct aag aac gca gtg gag gaa 2592
 Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val Glu Glu
 850 855 860

tat gtg tat gaa atg aga gac aag ctt agt ggt gaa tat gag aag ttt 2640
 Tyr Val Tyr Glu Met Arg Asp Lys Leu Ser Gly Glu Tyr Glu Lys Phe
 865 870 875 880

gtg agt gaa gat gat cgt aac agt ttt act ttg aaa ctg gaa gat act 2688
 Val Ser Glu Asp Asp Arg Asn Ser Phe Thr Leu Lys Leu Glu Asp Thr
 885 890 895

gaa aat tgg ttg tat gag gat gga gaa gac cag cca aag caa gtt tat 2736
 Glu Asn Trp Leu Tyr Glu Asp Gly Glu Asp Gln Pro Lys Gln Val Tyr
 900 905 910

gtt gat aag ttg gct gaa tta aaa aat cta ggt caa cct att aag ata 2784
 Val Asp Lys Leu Ala Glu Leu Lys Asn Leu Gly Gln Pro Ile Lys Ile
 915 920 925

cgt ttc cag gaa tct gaa gaa cga cca aat tat ttg aag 2823
 Arg Phe Gln Glu Ser Glu Glu Arg Pro Asn Tyr Leu Lys
 930 935 940

<210> 172

<211> 941

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP-HSP70

<400> 172

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

165	170	175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180	185	190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195	200	205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210	215	220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225	230	235
Gly Met Ser Val Val Gly Ile Asp Leu Gly Phe Gln Ser Cys Tyr Val 245	250	255
Ala Val Ala Arg Ala Gly Gly Ile Glu Thr Ile Ala Asn Glu Tyr Ser 260	265	270
Asp Arg Cys Thr Pro Ala Cys Ile Ser Phe Gly Pro Lys Asn Arg Ser 275	280	285
Ile Gly Ala Ala Ala Lys Ser Gln Val Ile Ser Asn Ala Lys Asn Thr 290	295	300
Val Gln Gly Phe Lys Arg Phe His Gly Arg Ala Phe Ser Asp Pro Phe 305	310	315
Val Glu Ala Glu Lys Ser Asn Leu Ala Tyr Asp Ile Val Gln Trp Pro 325	330	335
Thr Gly Leu Thr Gly Ile Lys Val Thr Tyr Met Glu Glu Glu Arg Asn 340	345	350
Phe Thr Thr Glu Gln Val Thr Ala Met Leu Leu Ser Lys Leu Lys Glu 355	360	365
Thr Ala Glu Ser Val Leu Lys Lys Pro Val Val Asp Cys Val Val Ser 370	375	380
Val Pro Cys Phe Tyr Thr Asp Ala Glu Arg Arg Ser Val Met Asp Ala 385	390	395
Thr Gln Ile Ala Gly Leu Asn Cys Leu Arg Leu Met Asn Glu Thr Thr 405	410	415
Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Arg Leu 420	425	430
Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met Gly His Ser Ala 435	440	445
Tyr Gln Val Ser Val Cys Ala Phe Asn Arg Gly Lys Leu Lys Val Leu 450	455	460
Ala Thr Ala Phe Asp Thr Thr Leu Gly Gly Arg Lys Phe Asp Glu Val		

465	470	475	480
Leu Val Asn His Phe Cys Glu Glu Phe Gly Lys Lys Tyr Lys Leu Asp			
485		490	495
Ile Lys Ser Lys Ile Arg Ala Leu Leu Arg Leu Ser Gln Glu Cys Glu			
500		505	510
Lys Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp Leu Pro Leu Ser			
515		520	525
Ile Glu Cys Phe Met Asn Asp Val Asp Val Ser Gly Thr Met Asn Arg			
530		535	540
Gly Lys Phe Leu Glu Met Cys Asn Asp Leu Leu Ala Arg Val Glu Pro			
545		550	555
Pro Leu Arg Ser Val Leu Glu Gln Thr Lys Leu Lys Lys Glu Asp Ile			
565		570	575
Tyr Ala Val Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys			
580		585	590
Glu Lys Ile Ser Lys Phe Phe Gly Lys Glu Leu Ser Thr Thr Leu Asn			
595		600	605
Ala Asp Glu Ala Val Thr Arg Gly Cys Ala Leu Gln Cys Ala Ile Leu			
610		615	620
Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Ile Thr Asp Val Val Pro			
625		630	635
640			
Tyr Pro Ile Ser Leu Arg Trp Asn Ser Pro Ala Glu Glu Gly Ser Ser			
645		650	655
Asp Cys Glu Val Phe Ser Lys Asn His Ala Ala Pro Phe Ser Lys Val			
660		665	670
Leu Thr Phe Tyr Arg Lys Glu Pro Phe Thr Leu Glu Ala Tyr Tyr Ser			
675		680	685
Ser Pro Gln Asp Leu Pro Tyr Pro Asp Pro Ala Ile Ala Gln Phe Ser			
690		695	700
Val Gln Lys Val Thr Pro Gln Ser Asp Gly Ser Ser Ser Lys Val Lys			
705		710	715
720			
Val Lys Val Arg Val Asn Val His Gly Ile Phe Ser Val Ser Ser Ala			
725		730	735
Ser Leu Val Glu Val His Lys Ser Glu Glu Asn Glu Glu Pro Met Glu			
740		745	750
Thr Asp Gln Asn Ala Lys Glu Glu Glu Lys Met Gln Val Asp Gln Glu			
755		760	765
Glu Pro His Val Glu Glu Gln Gln Gln Thr Pro Ala Glu Asn Lys			

770	775	780
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Ala Glu Ser Glu Glu Met Glu Thr Ser Gln Ala Gly Ser Lys Asp Lys	790	795
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Lys Met Asp Gln Pro Pro Gln Cys Gln Glu Gly Lys Ser Glu Asp Gln	805	810
---	-----	-----

Tyr Cys Gly Pro Ala Asn Arg Glu Ser Ala Ile Trp Gln Ile Asp Arg	820	825
---	-----	-----

Glu Met Leu Asn Leu Tyr Ile Glu Asn Glu Gly Lys Met Ile Met Gln	835	840
---	-----	-----

Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val Glu Glu	850	855
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Tyr Val Tyr Glu Met Arg Asp Lys Leu Ser Gly Glu Tyr Glu Lys Phe	865	870
---	-----	-----

Val Ser Glu Asp Asp Arg Asn Ser Phe Thr Leu Lys Leu Glu Asp Thr	885	890
---	-----	-----

Glu Asn Trp Leu Tyr Glu Asp Gly Glu Asp Gln Pro Lys Gln Val Tyr	900	905
---	-----	-----

Val Asp Lys Leu Ala Glu Leu Lys Asn Leu Gly Gln Pro Ile Lys Ile	915	920
---	-----	-----

Arg Phe Gln Glu Ser Glu Glu Arg Pro Asn Tyr Leu Lys	930	935
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940

<210> 173

<211> 2674

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP-HSC70

<220>

<221> CDS

<222> (1)..(2673)

<400> 173

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	1	5	10	15	48
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	20	25	30	96
---	----	----	----	----

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	35	40	45	144
---	----	----	----	-----

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192		
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag	240		
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys			
65	70	75	80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288		
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336		
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384		
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432		
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480		
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528		
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
gtg cag ctc gcc gac cac tac cag aac acc ccc atc ggc gac ggc	576		
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
180	185	190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624		
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
195	200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672		
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
210	215	220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc	720		
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
225	230	235	240
gga ctc aga tct atg tcc aag gga cct gca gtt ggt att gat ctt ggc	768		
Gly Leu Arg Ser Met Ser Lys Gly Pro Ala Val Gly Ile Asp Leu Gly			
245	250	255	
acc acc tac tct tgt gtg ggt gtt ttc cag cac gga aaa gtc gag ata	816		
Thr Thr Tyr Ser Cys Val Gly Val Phe Gln His Gly Lys Val Glu Ile			
260	265	270	

att gcc aat gat cag gga aac cga acc act cca agc tat gtc gcc ttt Ile Ala Asn Asp Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe 275 280 285	864
acg gac act gaa cgg ttg atc ggt gat gcc gca aag aat caa gtt gca Thr Asp Thr Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala 290 295 300	912
atg aac ccc acc aac aca gtt ttt gat gcc aaa cgt ctg att gga cgc Met Asn Pro Thr Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg 305 310 315 320	960
aga ttt gat gat gct gtt gtc cag tct gat atg aaa cat tgg ccc ttt Arg Phe Asp Asp Ala Val Val Gln Ser Asp Met Lys His Trp Pro Phe 325 330 335	1008
atg gtg gtg aat gat gct ggc agg ccc aag gtc caa gta gaa tac aag Met Val Val Asn Asp Ala Gly Arg Pro Lys Val Gln Val Glu Tyr Lys 340 345 350	1056
gga gag acc aaa agc ttc tat cca gag gag gtg tct tct atg gtt ctg Gly Glu Thr Lys Ser Phe Tyr Pro Glu Glu Val Ser Ser Met Val Leu 355 360 365	1104
aca aag atg aag gaa att gca gaa gcc tac ctt ggg aag act gtt acc Thr Lys Met Lys Glu Ile Ala Glu Ala Tyr Leu Gly Lys Thr Val Thr 370 375 380	1152
aat gct gtg gtc aca gtg cca gct tac ttt aat gac tct cag cgt cag Asn Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln 385 390 395 400	1200
gct acc aaa gat gct gga act att gct ggt ctc aat gta ctt aga att Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn Val Leu Arg Ile 405 410 415	1248
att aat gag cca act gct gct att gct tac ggc tta gac aaa aag Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys 420 425 430	1296
gtt gga gca gaa aga aac gtg ctc atc ttt gac ctg gga ggt ggc act Val Gly Ala Glu Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr 435 440 445	1344
ttt gat gtg tca atc ctc act att gag gat gga atc ttt gag gtc aag Phe Asp Val Ser Ile Leu Thr Ile Glu Asp Gly Ile Phe Glu Val Lys 450 455 460	1392
tct aca gct gga gac acc cac ttg ggt gga gaa gat ttt gac aac cga Ser Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg 465 470 475 480	1440
atg gtc aac cat ttt att gct gag ttt aag cgc aag cat aag aag gac Met Val Asn His Phe Ile Ala Glu Phe Lys Arg Lys His Lys Lys Asp 485 490 495	1488
atc agt gag aac aag aga gct gta aga cgc ctc cgt act gct tgt gaa	1536

Ile Ser Glu Asn Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu			
500	505	510	
cgt gct aag cgt acc ctc tct tcc agc acc cag gcc agt att gag atc		1584	
Arg Ala Lys Arg Thr Leu Ser Ser Ser Thr Gln Ala Ser Ile Glu Ile			
515	520	525	
gat tct ctc tat gaa gga atc gac ttc tat acc tcc att acc cgt gcc		1632	
Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala			
530	535	540	
cga ttt gaa gaa ctg aat gct gac ctg ttc cgt ggc acc ctg gac cca		1680	
Arg Phe Glu Glu Leu Asn Ala Asp Leu Phe Arg Gly Thr Leu Asp Pro			
545	550	555	560
gta gag aaa gcc ctt cga gat gcc aaa cta gac aag tca cag att cat		1728	
Val Glu Lys Ala Leu Arg Asp Ala Lys Leu Asp Lys Ser Gln Ile His			
565	570	575	
gat att gtc ctg gtt ggt ggt tct act cgt atc ccc aag att cag aag		1776	
Asp Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys Ile Gln Lys			
580	585	590	
ctt ctc caa gac ttc ttc aat gga aaa gaa ctg aat aag agc atc aac		1824	
Leu Leu Gln Asp Phe Phe Asn Gly Lys Glu Leu Asn Lys Ser Ile Asn			
595	600	605	
cct gat gaa gct gtt gct tat ggt gca gct gtc cag gca gcc atc ttg		1872	
Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Ile Leu			
610	615	620	
tct gga gac aag tct gag aat gtt caa gat ttg ctg ctc ttg gat gtc		1920	
Ser Gly Asp Lys Ser Glu Asn Val Gln Asp Leu Leu Leu Asp Val			
625	630	635	640
act cct ctt tcc ctt ggt att gaa act gct ggt gga gtc atg act gtc		1968	
Thr Pro Leu Ser Leu Gly Ile Glu Thr Ala Gly Gly Val Met Thr Val			
645	650	655	
ctc atc aag cgt aat acc acc att cct acc aag cag aca cag acc ttc		2016	
Leu Ile Lys Arg Asn Thr Thr Ile Pro Thr Lys Gln Thr Gln Thr Phe			
660	665	670	
act acc tat tct gac aac cag cct ggt gtg ctt att cag gtt tat gaa		2064	
Thr Thr Tyr Ser Asp Asn Gln Pro Gly Val Leu Ile Gln Val Tyr Glu			
675	680	685	
ggc gag cgt gcc atg aca aag gat aac aac ctg ctt ggc aag ttt gaa		2112	
Gly Glu Arg Ala Met Thr Lys Asp Asn Asn Leu Leu Gly Lys Phe Glu			
690	695	700	
ctc aca ggc ata cct cct gca ccc cga ggt gtt cct cag att gaa gtc		2160	
Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val			
705	710	715	720
act ttt gac att gat gcc aat ggt ata ctc aat gtc tct gct gtg gac		2208	
Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser Ala Val Asp			

725

730

735

aag agt acg gga aaa gag aac aag att act atc act aat gac aag ggc Lys Ser Thr Gly Lys Glu Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly 740	745	750	2256
cgt ttg agc aag gaa gac att gaa cgt atg gtc cag gaa gct gag aag Arg Leu Ser Lys Glu Asp Ile Glu Arg Met Val Gln Glu Ala Glu Lys 755	760	765	2304
tac aaa gct gaa gat gag aag cag agg gac aag gtg tca tcc aag aat Tyr Lys Ala Glu Asp Glu Lys Gln Arg Asp Lys Val Ser Ser Lys Asn 770	775	780	2352
tca ctt gag tcc tat gcc ttc aac atg aaa gca act gtt gaa gat gag Ser Leu Glu Ser Tyr Ala Phe Asn Met Lys Ala Thr Val Glu Asp Glu 785	790	795	2400
aaa ctt caa ggc aag att aac gat gag gac aaa cag aag att ctg gac Lys Leu Gln Gly Lys Ile Asn Asp Glu Asp Lys Gln Lys Ile Leu Asp 805	810	815	2448
aag tgt aat gaa att atc aac tgg ctt gat aag aat cag act gct gag Lys Cys Asn Glu Ile Ile Asn Trp Leu Asp Lys Asn Gln Thr Ala Glu 820	825	830	2496
aag gaa gaa ttt gaa cat caa cag aaa gag ctg gag aaa gtt tgc aac Lys Glu Glu Phe Glu His Gln Gln Lys Glu Leu Glu Lys Val Cys Asn 835	840	845	2544
ccc atc atc acc aag ctg tac cag agt gca gga ggc atg cca gga gga Pro Ile Ile Thr Lys Leu Tyr Gln Ser Ala Gly Gly Met Pro Gly Gly 850	855	860	2592
atg cct ggg gga ttt cct ggt ggt gga gct cct ccc tct ggt ggt gct Met Pro Gly Gly Phe Pro Gly Gly Ala Pro Pro Ser Gly Gly Ala 865	870	875	2640
tcc tca ggg ccc acc att gaa gag gtt gat taa g Ser Ser Gly Pro Thr Ile Glu Glu Val Asp 885	890		2674

<210> 174

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP-HSC70

<400> 174

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Leu Arg Ser Met Ser Lys Gly Pro Ala Val Gly Ile Asp Leu Gly
245 250 255

Thr Thr Tyr Ser Cys Val Gly Val Phe Gln His Gly Lys Val Glu Ile
260 265 270

Ile Ala Asn Asp Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe
275 280 285

Thr Asp Thr Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala
290 295 300

Met Asn Pro Thr Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg
305 310 315 320

Arg Phe Asp Asp Ala Val Val Gln Ser Asp Met Lys His Trp Pro Phe
325 330 335

Met Val Val Asn Asp Ala Gly Arg Pro Lys Val Gln Val Glu Tyr Lys
340 345 350

Gly Glu Thr Lys Ser Phe Tyr Pro Glu Glu Val Ser Ser Met Val Leu
355 360 365

Thr Lys Met Lys Glu Ile Ala Glu Ala Tyr Leu Gly Lys Thr Val Thr
370 375 380

Asn Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln
385 390 395 400

Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn Val Leu Arg Ile
405 410 415

Ile Asn Glu Pro Thr Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys
420 425 430

Val Gly Ala Glu Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Thr
435 440 445

Phe Asp Val Ser Ile Leu Thr Ile Glu Asp Gly Ile Phe Glu Val Lys
450 455 460

Ser Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg
465 470 475 480

Met Val Asn His Phe Ile Ala Glu Phe Lys Arg Lys His Lys Lys Asp
485 490 495

Ile Ser Glu Asn Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu
500 505 510

Arg Ala Lys Arg Thr Leu Ser Ser Ser Thr Gln Ala Ser Ile Glu Ile
515 520 525

Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala
530 535 540

Arg Phe Glu Glu Leu Asn Ala Asp Leu Phe Arg Gly Thr Leu Asp Pro
545 550 555 560

Val Glu Lys Ala Leu Arg Asp Ala Lys Leu Asp Lys Ser Gln Ile His
565 570 575

Asp Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys Ile Gln Lys
580 585 590

Leu Leu Gln Asp Phe Phe Asn Gly Lys Glu Leu Asn Lys Ser Ile Asn
595 600 605

Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Ile Leu
610 615 620

Ser Gly Asp Lys Ser Glu Asn Val Gln Asp Leu Leu Leu Asp Val
625 630 635 640

Thr Pro Leu Ser Leu Gly Ile Glu Thr Ala Gly Gly Val Met Thr Val
645 650 655

Leu Ile Lys Arg Asn Thr Thr Ile Pro Thr Lys Gln Thr Gln Thr Phe
660 665 670

Thr Thr Tyr Ser Asp Asn Gln Pro Gly Val Leu Ile Gln Val Tyr Glu
675 680 685

Gly Glu Arg Ala Met Thr Lys Asp Asn Asn Leu Leu Gly Lys Phe Glu
690 695 700

Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
705 710 715 720

Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser Ala Val Asp
725 730 735

Lys Ser Thr Gly Lys Glu Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly
740 745 750

Arg Leu Ser Lys Glu Asp Ile Glu Arg Met Val Gln Glu Ala Glu Lys
755 760 765

Tyr Lys Ala Glu Asp Glu Lys Gln Arg Asp Lys Val Ser Ser Lys Asn
770 775 780

Ser Leu Glu Ser Tyr Ala Phe Asn Met Lys Ala Thr Val Glu Asp Glu
785 790 795 800

Lys Leu Gln Gly Lys Ile Asn Asp Glu Asp Lys Gln Lys Ile Leu Asp
805 810 815

Lys Cys Asn Glu Ile Ile Asn Trp Leu Asp Lys Asn Gln Thr Ala Glu
820 825 830

Lys Glu Glu Phe Glu His Gln Gln Lys Glu Leu Glu Lys Val Cys Asn
835 840 845

Pro Ile Ile Thr Lys Leu Tyr Gln Ser Ala Gly Gly Met Pro Gly Gly
850 855 860

Met Pro Gly Gly Phe Pro Gly Gly Ala Pro Pro Ser Gly Gly Ala
865 870 875 880

Ser Ser Gly Pro Thr Ile Glu Glu Val Asp
885 890

<210> 175
<211> 2458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GFP-HSF1

<220>
 <221> CDS
 <222> (1) .. (2349)

<400> 175

atg	gtg	agc	aag	ggc	gac	gag	gag	ctg	tgc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu			
1	5										10				15			

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30 96

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45 144

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60 192

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80 240

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95 288

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110 336

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125 384

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140 432

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aac
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160 480

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175 528

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc gcc gac ggc
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190 576

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205 624

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	672
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	720
225 230 235 240	
gga ctc aga tct cga gctcaa gct tcg aat tct gca gtc gag atg gat Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Glu Met Asp	768
245 250 255	
ctg ccc gtg ggc ccc ggc gcg ggg ccc agc aac gtc ccg gcc ttc Leu Pro Val Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro Ala Phe	816
260 265 270	
ctg acc aag ctg tgg acc ctc gtg agc gac ccg gac acc gac gcg ctc Leu Thr Lys Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp Ala Leu	864
275 280 285	
atc tgc tgg agc ccg agc ggg aac agc ttc cac gtg ttc gac cag ggc Ile Cys Trp Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp Gln Gly	912
290 295 300	
cag ttt gcc aag gag gtg ccc aag tac ttc aag cac aac aac atg Gln Phe Ala Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn Asn Met	960
305 310 315 320	
gcc agc ttc gtg ccg cag ctc aac atg tat ggc ttc ccg aaa gtg gtc Ala Ser Phe Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val	1008
325 330 335	
cac atc gag cag ggc ggc ctg gtc aag cca gag aga gac gac acg gag His Ile Glu Gln Gly Leu Val Lys Pro Glu Arg Asp Asp Thr Glu	1056
340 345 350	
ttc cag cac cca tgc ttc ctg cgt ggc cag gag cag ctc ctt gag aac Phe Gln His Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu Glu Asn	1104
355 360 365	
atc aag agg aaa gtg acc agt gtg tcc acc ctg aag agt gaa gac ata Ile Lys Arg Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu Asp Ile	1152
370 375 380	
aag atc cgc cag gac agc gtc acc aag ctg ctg acg gac gtg cag ctg Lys Ile Arg Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val Gln Leu	1200
385 390 395 400	
atg aag ggg aag cag gag tgc atg gac tcc aag ctc ctg gcc atg aag Met Lys Gly Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala Met Lys	1248
405 410 415	
cat gag aat gag gct ctg tgg cgg gag gtg gcc agc ctt ccg cag aag His Glu Asn Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg Gln Lys	1296
420 425 430	

cat gcc cag caa cag aaa gtc gtc aac aag ctc att cag ttc ctg atc His Ala Gln Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe Leu Ile 435 440 445	1344
tca ctg gtg cag tca aac cgg atc ctg ggg gtg aag aga aag atc ccc Ser Leu Val Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys Ile Pro 450 455 460	1392
ctg atg ctg aac gac agt ggc tca gca cat tcc atg ccc aag tat agc Leu Met Leu Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys Tyr Ser 465 470 475 480	1440
cgg cag ttc tcc ctg gag cac gtc cac ggc tcg ggc ccc tac tcg gcc Arg Gln Phe Ser Leu Glu His Val His Gly Ser Gly Pro Tyr Ser Ala 485 490 495	1488
ccc tcc cca gcc tac agc agc tcc agc ctc tac gcc cct gat gct gtg Pro Ser Pro Ala Tyr Ser Ser Ser Leu Tyr Ala Pro Asp Ala Val 500 505 510	1536
gcc agc tct gga ccc atc atc tcc gac atc acc gag ctg gct cct gcc Ala Ser Ser Gly Pro Ile Ile Ser Asp Ile Thr Glu Leu Ala Pro Ala 515 520 525	1584
agc ccc atg gcc tcc ccc ggc ggg agc ata gac gag agg ccc cta tcc Ser Pro Met Ala Ser Pro Gly Gly Ser Ile Asp Glu Arg Pro Leu Ser 530 535 540	1632
agc agc ccc ctg gtg cgt gtc aag gag gag ccc ccc agc ccg cct cag Ser Ser Pro Leu Val Arg Val Lys Glu Glu Pro Pro Ser Pro Pro Gln 545 550 555 560	1680
agc ccc cgg gta gag gag gcg agt ccc ggg cgc cca tct tcc gtg gac Ser Pro Arg Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser Val Asp 565 570 575	1728
acc ctc ttg tcc ccg acc gcc ctc att gac tcc atc ctg cgg gag agt Thr Leu Leu Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg Glu Ser 580 585 590	1776
gaa cct gcc ccc gcc tcc gtc aca gcc ctc acg gac gcc agg ggc cac Glu Pro Ala Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg Gly His 595 600 605	1824
acg gac acc gag ggc cgg cct ccc tcc ccc ccg ccc acc tcc acc cct Thr Asp Thr Glu Gly Arg Pro Pro Ser Pro Pro Thr Ser Thr Pro 610 615 620	1872
gaa aag tgc ctc agc gta gcc tgc ctg gac aag aat gag ctc agt gac Glu Lys Cys Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu Ser Asp 625 630 635 640	1920
cac ttg gat gct atg gac tcc aac ctg gat aac ctg cag acc atg ctg His Leu Asp Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr Met Leu 645 650 655	1968
agc agc cac ggc ttc agc gtg gac acc agt gcc ctg ctg gac ctg ttc	2016

Ser Ser His Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp Leu Phe			
660	665	670	
agc ccc tcg gtg acc gtg ccc gac atg agc ctg cct gac ctt gac agc		2064	
Ser Pro Ser Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu Asp Ser			
675	680	685	
agc ctg gcc agt atc caa gag ctc ctg tct ccc cag gag ccc ccc agg		2112	
Ser Leu Ala Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro Pro Arg			
690	695	700	
cct ccc gag gca gag aac agc agc ccg gat tca ggg aag cag ctg gtg		2160	
Pro Pro Glu Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln Leu Val			
705	710	715	720
cac tac aca gcg cag ccg ctg ttc ctg ctg gac ccc ggc tcc gtg gac		2208	
His Tyr Thr Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser Val Asp			
725	730	735	
acc ggg agc aac gac ctg ccg gtg ctg ttt gag ctg gga gag ggc tcc		2256	
Thr Gly Ser Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu Gly Ser			
740	745	750	
tac ttc tcc gaa ggg gac ggc ttc gcc gag gac ccc acc atc tcc ctg		2304	
Tyr Phe Ser Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile Ser Leu			
755	760	765	
ctg aca ggc tcg gag cct ccc aaa gcc aag gac ccc act gtc tcc		2349	
Leu Thr Gly Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val Ser			
770	775	780	
tagaggcccc ggaggagctg ggcagccgc ccaccccccac ccccaagtaca gggctggct		2409	
tggggaggca gggcagccctc gcggctttgg gcactggtgg gtcggccgg		2458	

<210> 176
<211> 783
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GFP-HSF1

<400> 176			
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240

 Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Glu Met Asp
 245 250 255

 Leu Pro Val Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro Ala Phe
 260 265 270

 Leu Thr Lys Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp Ala Leu
 275 280 285

 Ile Cys Trp Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp Gln Gly
 290 295 300

 Gln Phe Ala Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn Asn Met
 305 310 315 320

 Ala Ser Phe Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val
 325 330 335

 His Ile Glu Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp Thr Glu
 340 345 350

 Phe Gln His Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu Glu Asn
 355 360 365

Ile Lys Arg Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu Asp Ile
370 375 380

Lys Ile Arg Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val Gln Leu
385 390 395 400

Met Lys Gly Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala Met Lys
405 410 415

His Glu Asn Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg Gln Lys
420 425 430

His Ala Gln Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe Leu Ile
435 440 445

Ser Leu Val Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys Ile Pro
450 455 460

Leu Met Leu Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys Tyr Ser
465 470 475 480

Arg Gln Phe Ser Leu Glu His Val His Gly Ser Gly Pro Tyr Ser Ala
485 490 495

Pro Ser Pro Ala Tyr Ser Ser Ser Leu Tyr Ala Pro Asp Ala Val
500 505 510

Ala Ser Ser Gly Pro Ile Ile Ser Asp Ile Thr Glu Leu Ala Pro Ala
515 520 525

Ser Pro Met Ala Ser Pro Gly Gly Ser Ile Asp Glu Arg Pro Leu Ser
530 535 540

Ser Ser Pro Leu Val Arg Val Lys Glu Glu Pro Pro Ser Pro Pro Gln
545 550 555 560

Ser Pro Arg Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser Val Asp
565 570 575

Thr Leu Leu Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg Glu Ser
580 585 590

Glu Pro Ala Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg Gly His
595 600 605

Thr Asp Thr Glu Gly Arg Pro Pro Ser Pro Pro Pro Thr Ser Thr Pro
610 615 620

Glu Lys Cys Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu Ser Asp
625 630 635 640

His Leu Asp Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr Met Leu
645 650 655

Ser Ser His Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp Leu Phe
660 665 670

Ser Pro Ser Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu Asp Ser
 675 680 685

Ser Leu Ala Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro Pro Arg
 690 695 700

Pro Pro Glu Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln Leu Val
 705 710 715 720

His Tyr Thr Ala Gln Pro Leu Phe Leu Asp Pro Gly Ser Val Asp
 725 730 735

Thr Gly Ser Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu Gly Ser
 740 745 750

Tyr Phe Ser Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile Ser Leu
 755 760 765

Leu Thr Gly Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val Ser
 770 775 780

<210> 177

<211> 2416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP-NFKB

<220>

<221> CDS

<222> (1)..(2415)

<400> 177

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg		48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1	5														15		

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc		96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
20	25													30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
35	40													45			

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50	55													60			

ctg	acc	acc	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag		240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
65	70													80			

cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		

85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc	cgc gcc gag		336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc			576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
180	185	190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg			624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
195	200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc			672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
210	215	220	
gtg acc gcc gcc ggg atc act ctc gcc atg gac gag ctg tac aag tcc			720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
225	230	235	240
gga ctc aga tct cga gat ccg ccc ttc atg gac gaa ctg ttc ccc ctc			768
Gly Leu Arg Ser Arg Asp Pro Pro Phe Met Asp Glu Leu Phe Pro Leu			
245	250	255	
atc ttc ccg gca gag cca gcc cag gcc tct ggc ccc tat gtg gag atc			816
Ile Phe Pro Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile			
260	265	270	
att gag cag ccc aag cag cgg ggc atg cgc ttc cgc tac aag tgc gag			864
Ile Glu Gln Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu			
275	280	285	
ggg cgc tcc gcg ggc agc atc cca ggc gag agg agc aca gat acc acc			912
Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr			
290	295	300	
aag acc cac ccc acc atc aag atc aat ggc tac aca gga cca ggg aca			960
Lys Thr His Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr			
305	310	315	320

gtg cgc atc tcc ctg gtc acc aag gac cct cct cac cgg cct cac ccc Val Arg Ile Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro 325 330 335	1008
cac gag ctt gta gga aag gac tgc cgg gat ggc ttc tat gag gct gag His Glu Leu Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu 340 345 350	1056
ctc tgc ccg gac cgc tgc atc cac agt ttc cag aac ctg gga atc cag Leu Cys Pro Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln 355 360 365	1104
tgt gtg aag aag cgg gac ctg gag cag gct atc agt cag cgc atc cag Cys Val Lys Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln 370 375 380	1152
acc aac aac aac ccc ttc caa gtt cct ata gaa gag cag cgt ggg gac Thr Asn Asn Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp 385 390 395 400	1200
tac gac ctg aat gct gtg cgg ctc tgc ttc cag gtg aca gtg cgg gac Tyr Asp Leu Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp 405 410 415	1248
cca tca ggc agg ccc ctc cgc ctg ccg cct gtc ctt tct cat ccc atc Pro Ser Gly Arg Pro Leu Arg Leu Pro Pro Val Leu Ser His Pro Ile 420 425 430	1296
ttt gac aat cgt gcc ccc aac act gcc gag ctc aag atc tgc cga gtg Phe Asp Asn Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val 435 440 445	1344
aac cga aac tct ggc agc tgc ctc ggt ggg gat gag atc ttc cta ctg Asn Arg Asn Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu 450 455 460	1392
tgt gac aag gtg cag aaa gag gac att gag gtg tat ttc acg gga cca Cys Asp Lys Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro 465 470 475 480	1440
ggc tgg gag gcc cga ggc tcc ttt tcg caa gct gat gtg cac cga caa Gly Trp Glu Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln 485 490 495	1488
gtg gcc att gtg ttc cgg acc cct ccc tac gca gac ccc agc ctg cag Val Ala Ile Val Phe Arg Thr Pro Tyr Ala Asp Pro Ser Leu Gln 500 505 510	1536
gct cct gtg cgt gtc tcc atg cag ctg cgg cgg cct tcc gac cgg gag Ala Pro Val Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu 515 520 525	1584
ctc agt gag ccc atg gaa ttc cag tac ctg cca gat aca gac gat cgt Leu Ser Glu Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg 530 535 540	1632

cac	cg	att	gag	gag	aaa	cgt	aaa	agg	aca	tat	gag	acc	ttc	aag	agc	1680
His	Arg	Ile	Glu	Glu	Lys	Arg	Lys	Arg	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	
545			550			555			560							
atc	atg	aag	aag	agt	cct	ttc	agc	gga	ccc	acc	gac	ccc	cgg	cct	cca	1728
Ile	Met	Lys	Lys	Ser	Pro	Phe	Ser	Gly	Pro	Thr	Asp	Pro	Arg	Pro	Pro	
565			570			575										
cct	cga	cgc	att	gct	gtg	cct	tcc	cgc	agc	tca	gct	tct	gtc	ccc	aag	1776
Pro	Arg	Arg	Ile	Ala	Val	Pro	Ser	Arg	Ser	Ser	Ala	Ser	Val	Pro	Lys	
580			585			590										
cca	gca	ccc	cag	ccc	tat	ccc	ttt	acg	tca	tcc	ctg	agc	acc	atc	aac	1824
Pro	Ala	Pro	Gln	Pro	Tyr	Pro	Phe	Thr	Ser	Ser	Leu	Ser	Thr	Ile	Asn	
595			600			605										
tat	gat	gag	ttt	ccc	acc	atg	gtg	ttt	cct	tct	ggg	cag	atc	agc	cag	1872
Tyr	Asp	Glu	Phe	Pro	Thr	Met	Val	Phe	Pro	Ser	Gly	Gln	Ile	Ser	Gln	
610			615			620										
gcc	tcg	gcc	ttg	gcc	ccg	gcc	cct	ccc	caa	gtc	ctg	ccc	cag	gct	cca	1920
Ala	Ser	Ala	Leu	Ala	Pro	Ala	Pro	Pro	Gln	Val	Leu	Pro	Gln	Ala	Pro	
625			630			635			640							
gcc	cct	gcc	cct	gct	cca	gcc	atg	gta	tca	gct	ctg	gcc	cag	gcc	cca	1968
Ala	Pro	Ala	Pro	Ala	Pro	Ala	Met	Val	Ser	Ala	Leu	Ala	Gln	Ala	Pro	
645			650			655										
gcc	cct	gtc	cca	gtc	cta	gcc	cca	ggc	cct	cct	cag	gct	gtg	gcc	cca	2016
Ala	Pro	Val	Pro	Val	Leu	Ala	Pro	Gly	Pro	Pro	Gln	Ala	Val	Ala	Pro	
660			665			670										
cct	gcc	ccc	aag	ccc	acc	cag	gct	ggg	gaa	gga	acg	ctg	tca	gag	gcc	2064
Pro	Ala	Pro	Lys	Pro	Thr	Gln	Ala	Gly	Glu	Gly	Thr	Leu	Ser	Glu	Ala	
675			680			685										
ctg	ctg	cag	ctg	cag	ttt	gat	gat	gaa	gac	ctg	ggg	gcc	ttg	ctt	ggc	2112
Leu	Leu	Gln	Leu	Gln	Phe	Asp	Asp	Glu	Asp	Leu	Gly	Ala	Leu	Leu	Gly	
690			695			700										
aac	agc	aca	gac	cca	gct	gtg	ttc	aca	gac	ctg	gca	tcc	gtc	gac	aac	2160
Asn	Ser	Thr	Asp	Pro	Ala	Val	Phe	Thr	Asp	Leu	Ala	Ser	Val	Asp	Asn	
705			710			715			720							
tcc	gag	ttt	cag	cag	ctg	ctg	aac	cag	ggc	ata	cct	gtg	gcc	ccc	cac	2208
Ser	Glu	Phe	Gln	Gln	Leu	Leu	Asn	Gln	Gly	Ile	Pro	Val	Ala	Pro	His	
725			730			735										
aca	act	gag	ccc	atg	ctg	atg	gag	tac	cct	gag	gct	ata	act	cgc	cta	2256
Thr	Thr	Glu	Pro	Met	Leu	Met	Glu	Tyr	Pro	Glu	Ala	Ile	Thr	Arg	Leu	
740			745			750			755							
gtg	aca	gcc	cag	agg	ccc	ccc	gac	cca	gct	cct	gct	cca	ctg	ggg	gcc	2304
Val	Thr	Ala	Gln	Arg	Pro	Pro	Asp	Pro	Ala	Pro	Ala	Pro	Ieu	Gly	Ala	
755			760			765										
ccg	ggg	ctc	ccc	aat	ggc	ctc	ttt	tca	gga	gat	gaa	gac	ttc	tcc	tcc	2352

Pro Gly Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser
 770 775 780

att gcg gac atg gac ttc tca gcc ctg ctg agt cag atc agc tcc aag 2400
 Ile Ala Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser Lys
 785 790 795 800

ggc gaa ttc gaa gct t 2416
 Gly Glu Phe Glu Ala
 805

<210> 178

<211> 805

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP-NFKB

<400> 178

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240

 Gly Leu Arg Ser Arg Asp Pro Pro Phe Met Asp Glu Leu Phe Pro Leu
 245 250 255

 Ile Phe Pro Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile
 260 265 270

 Ile Glu Gln Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu
 275 280 285

 Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr
 290 295 300

 Lys Thr His Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr
 305 310 315 320

 Val Arg Ile Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro
 325 330 335

 His Glu Leu Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu
 340 345 350

 Leu Cys Pro Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln
 355 360 365

 Cys Val Lys Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln
 370 375 380

 Thr Asn Asn Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp
 385 390 395 400

 Tyr Asp Leu Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp
 405 410 415

 Pro Ser Gly Arg Pro Leu Arg Leu Pro Pro Val Leu Ser His Pro Ile
 420 425 430

 Phe Asp Asn Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val
 435 440 445

 Asn Arg Asn Ser Gly Ser Cys Leu Gly Asp Glu Ile Phe Leu Leu
 450 455 460

 Cys Asp Lys Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro
 465 470 475 480

 Gly Trp Glu Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln
 485 490 495

Val Ala Ile Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln
500 505 510

Ala Pro Val Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu
515 520 525

Leu Ser Glu Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg
530 535 540

His Arg Ile Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser
545 550 555 560

Ile Met Lys Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro
565 570 575

Pro Arg Arg Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys
580 585 590

Pro Ala Pro Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn
595 600 605

Tyr Asp Glu Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln
610 615 620

Ala Ser Ala Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro
625 630 635 640

Ala Pro Ala Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro
645 650 655

Ala Pro Val Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro
660 665 670

Pro Ala Pro Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala
675 680 685

Leu Leu Gln Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly
690 695 700

Asn Ser Thr Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn
705 710 715 720

Ser Glu Phe Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His
725 730 735

Thr Thr Glu Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu
740 745 750

Val Thr Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala
755 760 765

Pro Gly Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser
770 775 780

Ile Ala Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser Lys
785 790 795 800

Gly Glu Phe Glu Ala
805

<210> 179
<211> 1677
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GFP-IKB

<220>
<221> CDS
<222> (1) .. (1674)

<400> 179
atg ttc cag gcg gct gag cgc ccc cag gag tgg gcc atg gag ggc ccc 48
Met Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro
1 5 10 15

cgc gac ggg ctg aag aag gag cg_g cta ctg gac gac cgc cac gac agc 96
 Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His Asp Ser
 20 25 30

ggc ctg gac tcc atg aaa gac gag gag tac gag cag atg gtc aag gag 144
 Gly Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu
 35 40 45

ctg cag gag atc cgc ctc gag ccg cag gag gtg ccg cgc ggc tcg gag 192
 Leu Gln Glu Ile Arg Leu Glu Pro Gln Glu Val Pro Arg Gly Ser Glu
 50 55 60

ccc tgg aag cag cag ctc acc gag gac ggg gac tcg ttc ctg cac ttg 240
 Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu
 65 70 75 80

gcc atc atc cat gaa gaa aag gca ctg acc atg gaa gtg atc cgc cag 288
 Ala Ile Ile His Glu Glu Lys Ala Leu Thr Met Glu Val Ile Arg Gln
 85 90 95

gtg aag gga gac ctg gcc ttc ctc aac ctc cag aac aac ctg cag cag 336
 Val Lys Gly Asp Leu Ala Phe Leu Asn Leu Gln Asn Asn Leu Gln Gln
 100 105 110

act cca ctc cac ttg gct gtg atc acc aac cag cca gaa att gct gag 384
Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Glu Ile Ala Glu
115 120 125

gca ctt ctg gga gct ggc tgt gat cct gag ctc cga gac ttt cga gga 432
 Ala Leu Leu Gly Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly
 130 135 140

aat acc ccc cta cac ctt gcc tgt gag cag ggc tgc ctg gcc agc gtg	480
Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val	
145 150 155 160	

gga gtc ctg act cag tcc tgc acc acc ccg cac ctc cac tcc atc ttg Gly Val Leu Thr Gln Ser Cys Thr Thr Pro His Leu His Ser Ile Leu 165 170 175	528
aag gct acc aac tac aat ggc cac acg tgt cta cac tta gcc tct atc Lys Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile 180 185 190	576
cat ggc tac ctg ggc atc gtg gag ctt ttg gtg tcc ttg ggt gct gat His Gly Tyr Leu Gly Ile Val Glu Leu Leu Val Ser Leu Gly Ala Asp 195 200 205	624
gtc aat gct cag gag ccc tgt aat ggc cgg act gcc ctt cac ctc gca Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala 210 215 220	672
gtg gac ctg caa aat cct gac ctg gtg tca ctc ctg ttg aag tgt ggg Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly 225 230 235 240	720
gct gat gtc aac aga gtt acc tac cag ggc tat tct ccc tac cag ctc Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu 245 250 255	768
acc tgg ggc cgc cca agc acc cgg ata cag cag cag ctg ggc cag ctg Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Leu Gly Gln Leu 260 265 270	816
aca cta gaa aac ctt cag atg ctg cca gag agt gag gat gag gag agc Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser 275 280 285	864
tat gac aca gag tca gag ttc acg gag ttc aca gag gac gag ctg ccc Tyr Asp Thr Glu Ser Glu Phe Thr Glu Phe Thr Glu Asp Glu Leu Pro 290 295 300	912
tat gat gac tgt gtg ttt gga ggc cag cgt ctg acg tta acc ggt atg Tyr Asp Asp Cys Val Phe Gly Gly Gln Arg Leu Thr Leu Thr Gly Met 305 310 315 320	960
gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt gtt Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 325 330 335	1008
gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 340 345 350	1056
ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 355 360 365	1104
act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 370 375 380	1152
tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa cgg	1200

Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg				
385	390	395	400	
cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa agg				1248
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg				
405	410	415		
acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa gtc				1296
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val				
420	425	430		
aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att				1344
Lys Phe Glu Gly Asp Thr Leu Asn Arg Ile Glu Leu Lys Gly Ile				
435	440	445		
gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac aac				1392
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn				
450	455	460		
tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga				1440
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly				
465	470	475	480	
atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc gtt				1488
Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val				
485	490	495		
caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct				1536
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro				
500	505	510		
gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg				1584
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser				
515	520	525		
aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta				1632
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val				
530	535	540		
aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tag				1677
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn				
545	550	555		

<210> 180
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GFP-IKB

<400> 180
Met Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro
1 5 10 15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His Asp Ser

20	25	30
Gly Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu		
35	40	45
Leu Gln Glu Ile Arg Leu Glu Pro Gln Glu Val Pro Arg Gly Ser Glu		
50	55	60
Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu		
65	70	75
Ala Ile Ile His Glu Glu Lys Ala Leu Thr Met Glu Val Ile Arg Gln		
85	90	95
Val Lys Gly Asp Leu Ala Phe Leu Asn Leu Gln Asn Asn Leu Gln Gln		
100	105	110
Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Glu Ile Ala Glu		
115	120	125
Ala Leu Leu Gly Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly		
130	135	140
Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val		
145	150	155
Gly Val Leu Thr Gln Ser Cys Thr Thr Pro His Leu His Ser Ile Leu		
165	170	175
Lys Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile		
180	185	190
His Gly Tyr Leu Gly Ile Val Glu Leu Leu Val Ser Leu Gly Ala Asp		
195	200	205
Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala		
210	215	220
Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly		
225	230	235
Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu		
245	250	255
Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu		
260	265	270
Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser		
275	280	285
Tyr Asp Thr Glu Ser Glu Phe Thr Glu Phe Thr Glu Asp Glu Leu Pro		
290	295	300
Tyr Asp Asp Cys Val Phe Gly Gly Gln Arg Leu Thr Leu Thr Gly Met		
305	310	315
Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		

325	330	335
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
340	345	350
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
355	360	365
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
370	375	380
Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg		
385	390	395
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
405	410	415
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
420	425	430
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
435	440	445
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
450	455	460
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
465	470	475
Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val		
485	490	495
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
500	505	510
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
515	520	525
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
530	535	540
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn		
545	550	555